

SEQUENCE LISTING

<110> Barbet, Anthony F.
Whitmire, William M.
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Mahan, Suman M.

<120> Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides, and Methods of Use

<130> UF-299XC1

<150> US 60/269,944

<151> 2001-02-20

<160> 117

<170> PatentIn version 3.1

<210> 1

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<212> PRT

<213> Ehrlichia chaffeensis

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His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
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Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
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85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
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Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly
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Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu
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Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr
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Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly
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Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile
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Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
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Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro
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tccttaAGTA attactACTG ctaaataAAA tcgtAGCCTT ttatATGACT ctTTTTact	4080
atAGAAAATT caccaatcta acaatAGTAA ataaaaATTt tttaattttt atgacatttG	4140
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aaaaaaaaACTT ttttgtaAT agtcatattA atataACTT tagcaatata aatattGAAT	4260
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 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 Product="1hworfli"

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tttacCTTGA aattcttAA taattttATC atgtattGgt aataatCTAC tgtctttcTC	180

tatagatatt aatttttag gattttt gagtattgaa taagtcattg taccaagtcc	240
gggaccaatt tcaataattg aaaaattgct aatgtttcct gcataattaa ctatttatc	300
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Product="lhworf2"

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gaa gat aaa gta aag gta tta tgc cca cca ttt att gcg tta tct Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser	144
35 40 45	

act tat gtt aat tgt cca cat aat att aag ttt ggt gga cag aac tgt Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys	192
50 55 60	

tgt tat gta tct agt ggg aag tac act gga gaa att agt gct agt atg Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met	240
65 70 75 80	

tta tat aac tct gga tgt agt tat gta ata gtg ggt cac tct gaa agg Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg	288
85 90 95	

agg agt acg ttt cat gaa act gat cat gat gtt agg tta aaa gct gaa Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu	336
100 105 110	

tgt gcg atc gaa tca gga tta ata cca att att tgt gtt gga gaa act Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr	384
115 120 125	

tta cta gat agg gaa aat ggt atg cta aaa gat act tta tta agt caa Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln 130 135 140	432
tgt agt gaa tct ttt cct aaa aat ggt aag ttt atc ata gca tat gag Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu 145 150 155 160	480
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ata gaa gct tta gag att att agg tca tat gat tat gta tct gat atc Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile 180 185 190	576
ata tat ggt gga gca gta aat cat act aat gta ggt gat att gta agt Ile Tyr Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser 195 200 205	624
atc aat caa ttg tct ggt gtt tta gtt ggt agt gct agt tta gat atg Ile Asn Gln Leu Ser Gly Val Leu Val Gly Ser Ala Ser Leu Asp Met 210 215 220	672
gag agt ttt ttt aat ata ata tgt agt gct ata aat gtg agg caa agt Glu Ser Phe Phe Asn Ile Ile Cys Ser Ala Ile Asn Val Arg Gln Ser 225 230 235 240	720
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)	
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Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser 35 40 45	
Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys 50 55 60	

Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met
 65 70 75 80

Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg
 85 90 95

Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu
 100 105 110

Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr
 115 120 125

Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln
 130 135 140

Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu
 145 150 155 160

Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile
 165 170 175

Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile
 180 185 190

Ile Tyr Gly Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser
 195 200 205

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<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

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<223> Corresponds to SEQ ID NO:2, nucleotides 1333..2313
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Product="1hworf3"

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aat gct gcc att gct tca act gac tca tca gaa gat aaa cag tat att		96
Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile		
20 25 30		
tta att ggt act ggt tct atg act gga gta tat tat cct ata gga ggt		144
Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly		
35 40 45		
agc ata tgt agg ttt att gca tct gat tat ggt aat gat aat aac agc		192
Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser		
50 55 60		
ata gtt tgt tct ata tct tct aca act ggt agc gta tat aat ctt aat		240
Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn		
65 70 75 80		
tct atg cgt tat gca aat atg gat ata ggt att att caa tct gat tta		288
Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu		
85 90 95		
gag tac tat gca tat aat ggt att ggt tta tat gaa aaa atg cca gca		336
Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala		
100 105 110		
atg agg cat cta aga ata tta tct tca tta cat aaa gaa tat ctt aca		384
Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr		
115 120 125		
att gtt gtt agg gcg aat tct aat ata tca gtt att gat gat ata aaa		432
Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys		
130 135 140		
ggc aaa aga gtt aat att ggt agt cct ggt act ggt gta aga ata gca		480
Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala		
145 150 155 160		
atg tta aaa ttg tta aat gaa aaa gga tgg gga aga aaa gat ttt gct		528
Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala		
165 170 175		
gtt atg gca gaa tta aaa tca tca gag caa gct caa gca tta tgt gat		576
Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp		
180 185 190		
aat aaa att gat gtg atg gta gat gtt ggt gga cat cct aat gct gca		624
Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala		
195 200 205		

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gat att att agt ggt gcg tta tac agt aac tta cct gat ata caa act Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr 245 250 255	768
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cag tca gat att aca cct tta cat gac ggt gca aaa cgt tat tat aag Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys 305 310 315 320	960
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Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser 50 55 60	

Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn
65 70 75 80

Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu
85 90 95

Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala
100 105 110

Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr
115 120 125

Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys
130 135 140

Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala
145 150 155 160

Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala
165 170 175

Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp
180 185 190

Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala
195 200 205

Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp
210 215 220

Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg
225 230 235 240

Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr
245 250 255

Val Ser Val Lys Ala Ser Leu Ile Thr Thr Glu Leu Ser Asn Glu
260 265 270

Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu
275 280 285

His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val
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<212> DNA

<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

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<222> (1) .. (756)

<223> Corresponds to SEQ ID NO:2, nucleotides 2611..3366
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 Product="1hworf4"

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Val Asn His Leu Glu Ala His Thr Leu Leu Ile Arg Met Phe His Asp	
20 25 30	

att gat ttt cca ttt tta gta ttg atc ata tct ggc gga cat tgt cag	144
Ile Asp Phe Pro Phe Leu Val Leu Ile Ile Ser Gly Gly His Cys Gln	
35 40 45	

ttt tta ata gtt cat gat gtt gga tgt tat caa aga tta ggt tct tct	192
Phe Leu Ile Val His Asp Val Gly Cys Tyr Gln Arg Leu Gly Ser Ser	
50 55 60	

tta gat gac tcc ctt ggt gaa gta ttt gat aaa gta gca aga atg ttg	240
Leu Asp Asp Ser Leu Gly Glu Val Phe Asp Lys Val Ala Arg Met Leu	
65 70 75 80	

aat ttg gga tat cct gga ggg cca att att gaa aaa aaa tcc ata atg	288
Asn Leu Gly Tyr Pro Gly Gly Pro Ile Ile Glu Lys Lys Ser Ile Met	
85 90 95	

ggt gat agc aaa agt ttt ttt cta cca cgt gca tta atc aat cgt ctt	336
Gly Asp Ser Lys Ser Phe Phe Leu Pro Arg Ala Leu Ile Asn Arg Leu	
100 105 110	

gga tgt gat ttt tct ttc tcc ggt att aag acg gca gta aga aat att Gly Cys Asp Phe Ser Phe Ser Gly Ile Lys Thr Ala Val Arg Asn Ile 115 120 125	384
gtt gta aat caa aaa tat ata gat aat gat ttt ata tgt aat att tca Val Val Asn Gln Lys Tyr Ile Asp Asn Asp Phe Ile Cys Asn Ile Ser 130 135 140	432
gct tct ttt caa gat tgt att ggt gat ata tta gta aac agg att act Ala Ser Phe Gln Asp Cys Ile Gly Asp Ile Leu Val Asn Arg Ile Thr 145 150 155 160	480
aat gct att cat atg tca caa gct ata aat tgt aag att aat aag tta Asn Ala Ile His Met Ser Gln Ala Ile Asn Cys Lys Ile Asn Lys Leu 165 170 175	528
gta gta act gga ggt gtt gca gct aat cac cta tta cgt aat cgt ata Val Val Thr Gly Gly Val Ala Ala Asn His Leu Leu Arg Asn Arg Ile 180 185 190	576
tca att tgt gta aaa gat aat aat ttt gag gtg cta tat cct cca act Ser Ile Cys Val Lys Asp Asn Asn Phe Glu Val Leu Tyr Pro Pro Thr 195 200 205	624
gag tta tgt act gat aat gga att atg gtt ggg tgg gct ggt att gaa Glu Leu Cys Thr Asp Asn Gly Ile Met Val Gly Trp Ala Gly Ile Glu 210 215 220	672
aat tta tct aaa ggt tat gtt tct aat tta gat ttt gtt cca aaa gca Asn Leu Ser Lys Gly Tyr Val Ser Asn Leu Asp Phe Val Pro Lys Ala 225 230 235 240	720
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<210> 9
<211> 251
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 9

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1 5 10 15

Val Asn His Leu Glu Ala His Thr Leu Leu Ile Arg Met Phe His Asp
20 25 30

Ile Asp Phe Pro Phe Leu Val Leu Ile Ile Ser Gly Gly His Cys Gln
35 40 45

Phe Leu Ile Val His Asp Val Gly Cys Tyr Gln Arg Leu Gly Ser Ser
50 55 60

Leu Asp Asp Ser Leu Gly Glu Val Phe Asp Lys Val Ala Arg Met Leu
65 70 75 80

Asn Leu Gly Tyr Pro Gly Gly Pro Ile Ile Glu Lys Lys Ser Ile Met
85 90 95

Gly Asp Ser Lys Ser Phe Phe Leu Pro Arg Ala Leu Ile Asn Arg Leu
100 105 110

Gly Cys Asp Phe Ser Phe Ser Gly Ile Lys Thr Ala Val Arg Asn Ile
115 120 125

Val Val Asn Gln Lys Tyr Ile Asp Asn Asp Phe Ile Cys Asn Ile Ser
130 135 140

Ala Ser Phe Gln Asp Cys Ile Gly Asp Ile Leu Val Asn Arg Ile Thr
145 150 155 160

Asn Ala Ile His Met Ser Gln Ala Ile Asn Cys Lys Ile Asn Lys Leu
165 170 175

Val Val Thr Gly Gly Val Ala Ala Asn His Leu Leu Arg Asn Arg Ile
180 185 190

Ser Ile Cys Val Lys Asp Asn Asn Phe Glu Val Leu Tyr Pro Pro Thr
195 200 205

Glu Leu Cys Thr Asp Asn Gly Ile Met Val Gly Trp Ala Gly Ile Glu
210 215 220

Asn Leu Ser Lys Gly Tyr Val Ser Asn Leu Asp Phe Val Pro Lys Ala
225 230 235 240

Arg Trp Pro Leu Glu Ser Ile Lys Arg Ser Ser
245 250

<210> 10

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<211> 222
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<220>
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<222> (1)..(222)
<223> Corresponds to SEQ ID NO:2, nucleotides 4065..4286
Product="lhwarf5"

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aaa aat ttt tta att tat atg aca ttt gta tat tac tat aaa tca gta 96
Lys Asn Phe Leu Ile Tyr Met Thr Phe Val Tyr Tyr Lys Ser Val
20 25 30

ttt att aaa gtt aag aat att aat gta ttt aag ttt aaa aaa aac 144
Phe Ile Lys Val Lys Asn Ile Asn Asn Val Phe Lys Phe Lys Lys Asn
35 40 45

ttt ttt gta aat agt cat att aat ata act ttt agc aat ata aat att 192
Phe Phe Val Asn Ser His Ile Asn Ile Thr Phe Ser Asn Ile Asn Ile
50 55 60

gaa ttt tca gta ctt acg tca tac tgt taa 222
Glu Phe Ser Val Leu Thr Ser Tyr Cys
65 70

<210> 11
<211> 73
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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Lys Asn Phe Leu Ile Tyr Met Thr Phe Val Tyr Tyr Lys Ser Val
20 25 30

Phe Ile Lys Val Lys Asn Ile Asn Asn Val Phe Lys Phe Lys Lys Asn
35 40 45

Phe Phe Val Asn Ser His Ile Asn Ile Thr Phe Ser Asn Ile Asn Ile
50 55 60

Glu Phe Ser Val Leu Thr Ser Tyr Cys
 65 70

<210> 12
<211> 4913
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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aaaaaaaggta agattatgaa tatattcaat tatatgcaga taatgcctaa tataagtgtt	240
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attgaaatgt taacattatt gaatgtttt cttgttaatta tacgttaatg tataggttat	3060
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aacaaagcca caaaataatg atcttagatataat tcatgatact gataaagaga aattaataca	4260
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gaagcttagt aattctgatt tttatgcaat tgatatttg ttattagaat taatattggt 4680
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 aatggtgcaa ttattccgtg atttattatc tgcaagacaa agtatggtgt taggtgattt 4860
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<210> 13
 <211> 519
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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 <222> (1)..(519)
 <223> Corresponds to SEQ ID NO:12, nucleotides 196..714
 Hypothetical ferripyochelin binding protein
 Product="4hworf1"

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 Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp
 1 5 10 15
 gca ttt gtt gca cct act gct gta att ata ggt gat gtt tgt gta aat 96
 Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn
 20 25 30
 gac aag tgt agc att tgg tat aac tca gta tta cgt gga gat gta ggc 144
 Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly
 35 40 45
 caa att gtt att ggt gta ggt act aat att caa gat ggg aca ata ata 192
 Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile
 50 55 60
 cat gtt gat agg aaa tat ggt aat acg aat att ggc aaa aag gtt act 240
 His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr
 65 70 75 80
 att ggg cat ggg tgt ata tta cat gct tgt gag ata caa gat tat gtg 288
 Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val
 85 90 95
 ctt gtt gga atg gga tct att att atg gat aac gtt gtg gtt gaa aag 336
 Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys
 100 105 110
 aat gca atg gtg gct ggt gga tca tta gtg gta aga ggt aaa gtt gtg 384
 Asn Ala Met Val Ala Gly Ser Leu Val Val Arg Gly Lys Val Val

115

120

125

aaa act ggt gaa tta tgg gct ggt agg cct gca caa ttt tta aga atg
 Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met
 130 135 140

432

ttg tct agt gat gaa att aaa gag ata agt aaa tct gct gat aac tat
 Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
 145 150 155 160

480

ata gag ctt gcc agt gat tac ata act ggt aag ttg taa
 Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
 165 170

519

<210> 14

<211> 172

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp
 1 5 10 15

Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn
 20 25 30

Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly
 35 40 45

Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile
 50 55 60

His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr
 65 70 75 80

Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val
 85 90 95

Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys
 100 105 110

Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val
 115 120 125

Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met

Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
 145 150 155 160

Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
165 170

<210> 15
<211> 1209
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

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      Hypothetical dihydrolipoamide acetyltransferase
      Product="4hworf2"
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1 5 10 15

tta gaa gct cca att cga gtt tct gtt aag att ggt gat agt att aag 96
 Leu Glu Ala Pro Ile Arg Val Ser Val Lys Ile Gly Asp Ser Ile Lys
 20 25 30

caa ggt gat gta ttg ttt atc att gaa acg gat aaa act tct cta gaa
 Gln Gly Asp Val Leu Phe Ile Ile Glu Thr Asp Lys Thr Ser Leu Glu
 35 40 45

att gta tct cct gta gat gga aca gtt agt aaa gta ttt ata gca gat 192
 Ile Val Ser Pro Val Asp Gly Thr Val Ser Lys Val Phe Ile Ala Asp
 50 55 60

gaa gaa att ata gaa cgt gat caa ctt tta tgt aca ata aat gtt ggt	240
Glu Glu Ile Ile Glu Arg Asp Gln Leu Leu Cys Thr Ile Asn Val Gly	
65 70 75 80	

gaa tta tca cat att gtc cag tct caa act cag gat cct aaa aca gat 288
 Glu Leu Ser His Ile Val Gln Ser Gln Thr Gln Asp Pro Lys Thr Asp
 85 90 95

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aat ggt gat att att aat gat gat att cag acg ttt ata cag aaa aaa 336
Asn Gly Asp Ile Ile Asn Asp Asp Ile Gln Thr Phe Ile Gln Lys Lys
          100           105           110

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gat gct cct tct gca gta aaa att atg gca gaa aat tca att gat aag 384
Asp Ala Pro Ser Ala Val Lys Ile Met Ala Glu Asn Ser Ile Asp Lys

115

120

125

aat cag atc aat ggg tct ggt att ggt gga aga att aca aaa tct gat Asn Gln Ile Asn Gly Ser Gly Ile Gly Gly Arg Ile Thr Lys Ser Asp 130 135 140	432
gtt tta gac cac att aat gtt gtt tca aaa gat cat agt gtg ctt tct Val Leu Asp His Ile Asn Val Val Ser Lys Asp His Ser Val Leu Ser 145 150 155 160	480
gaa caa tgt agt att act tct cat gag aag aga gaa gaa cgt gtt aag Glu Gln Cys Ser Ile Thr Ser His Glu Lys Arg Glu Glu Arg Val Lys 165 170 175	528
atg agt aaa att agg cag gtg att gct gcg agg ctt aag gag tct caa Met Ser Lys Ile Arg Gln Val Ile Ala Ala Arg Leu Lys Glu Ser Gln 180 185 190	576
aat act gct gca ata tta act acg ttt aat gaa gtg gat atg aag aat Asn Thr Ala Ala Ile Leu Thr Thr Phe Asn Glu Val Asp Met Lys Asn 195 200 205	624
gtt atg gat ctt cgt gtt cag tat agg gag acc ttt gaa aag aaa tat Val Met Asp Leu Arg Val Gln Tyr Arg Glu Thr Phe Glu Lys Lys Tyr 210 215 220	672
ggg gtc aaa ctt gga ttt atg tct ttt ata aaa gcg gta gta tta Gly Val Lys Leu Gly Phe Met Ser Phe Phe Ile Lys Ala Val Val Leu 225 230 235 240	720
gca tta aaa gaa tta cca gta att aat gct gag ata tct ggt aat gag Ala Leu Lys Glu Leu Pro Val Ile Asn Ala Glu Ile Ser Gly Asn Glu 245 250 255	768
att ata tat aaa cat tat tat gac ata ggt att gct gta ggg aca gac Ile Ile Tyr Lys His Tyr Tyr Asp Ile Gly Ile Ala Val Gly Thr Asp 260 265 270	816
aaa ggt cta gtt gtt cca gta atg cgt gat gct gat aag atg tct tgt Lys Gly Leu Val Val Pro Val Met Arg Asp Ala Asp Lys Met Ser Cys 275 280 285	864
gct gag ctt gag tta acc tta gct tct tta ggt aag aaa gct agg gaa Ala Glu Leu Glu Leu Thr Leu Ala Ser Leu Gly Lys Lys Ala Arg Glu 290 295 300	912
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aat ggt ggg gta tat ggt tca tta tta tct act cct ata att aat cct Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile Ile Asn Pro 325 330 335	1008
cct cag tct ggt att tta ggt atg cac tct ata caa aaa cga cca gta	1056

Pro Gln Ser Gly Ile Leu Gly Met His Ser Ile Gln Lys Arg Pro Val			
340	345	350	
gta gtt aat gat aat tct ata gag att aga cct atg atg tac att gca			1104
Val Val Asn Asp Asn Ser Ile Glu Ile Arg Pro Met Met Tyr Ile Ala			
355	360	365	
tta tct tat gat cat aga att gtt gat gga caa ggt gct gta aca ttt			1152
Leu Ser Tyr Asp His Arg Ile Val Asp Gly Gln Gly Ala Val Thr Phe			
370	375	380	
tta gta aga gtt aaa cag tat att gaa gat cca agt aga atg ttt cta			1200
Leu Val Arg Val Lys Gln Tyr Ile Glu Asp Pro Ser Arg Met Phe Leu			
385	390	395	400
gaa ata taa			1209
Glu Ile			
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)			
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Gl n Gly Asp Val Leu Phe Ile Ile Glu Thr Asp Lys Thr Ser Leu Glu			
35	40	45	
Ile Val Ser Pro Val Asp Gly Thr Val Ser Lys Val Phe Ile Ala Asp			
50	55	60	
Glu Glu Ile Ile Glu Arg Asp Gln Leu Leu Cys Thr Ile Asn Val Gly			
65	70	75	80
Glu Leu Ser His Ile Val Gln Ser Gln Thr Gln Asp Pro Lys Thr Asp			
85	90	95	
Asn Gly Asp Ile Ile Asn Asp Asp Ile Gln Thr Phe Ile Gln Lys Lys			
100	105	110	

Asp Ala Pro Ser Ala Val Lys Ile Met Ala Glu Asn Ser Ile Asp Lys
115 120 125

Asn Gln Ile Asn Gly Ser Gly Ile Gly Gly Arg Ile Thr Lys Ser Asp
130 135 140

Val Leu Asp His Ile Asn Val Val Ser Lys Asp His Ser Val Leu Ser
145 150 155 160

Glu Gln Cys Ser Ile Thr Ser His Glu Lys Arg Glu Glu Arg Val Lys
165 170 175

Met Ser Lys Ile Arg Gln Val Ile Ala Ala Arg Leu Lys Glu Ser Gln
180 185 190

Asn Thr Ala Ala Ile Leu Thr Thr Phe Asn Glu Val Asp Met Lys Asn
195 200 205

Val Met Asp Leu Arg Val Gln Tyr Arg Glu Thr Phe Glu Lys Lys Tyr
210 215 220

Gly Val Lys Leu Gly Phe Met Ser Phe Phe Ile Lys Ala Val Val Leu
225 230 235 240

Ala Leu Lys Glu Leu Pro Val Ile Asn Ala Glu Ile Ser Gly Asn Glu
245 250 255

Ile Ile Tyr Lys His Tyr Tyr Asp Ile Gly Ile Ala Val Gly Thr Asp
260 265 270

Lys Gly Leu Val Val Pro Val Met Arg Asp Ala Asp Lys Met Ser Cys
275 280 285

Ala Glu Leu Glu Leu Thr Leu Ala Ser Leu Gly Lys Lys Ala Arg Glu
290 295 300

Gly Lys Leu Glu Val Ser Asp Met Ala Gly Ala Thr Phe Thr Ile Thr
305 310 315 320

Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile Ile Asn Pro
325 330 335

Pro Gln Ser Gly Ile Leu Gly Met His Ser Ile Gln Lys Arg Pro Val
340 345 350

Val Val Asn Asp Asn Ser Ile Glu Ile Arg Pro Met Met Tyr Ile Ala
355 360 365

Leu Ser Tyr Asp His Arg Ile Val Asp Gly Gln Gly Ala Val Thr Phe
370 375 380

Leu Val Arg Val Lys Gln Tyr Ile Glu Asp Pro Ser Arg Met Phe Leu
 385 390 395 400

Glu Ile

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<210> 17
<211> 1227
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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<220>
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<222> (1)..(1227)
<223> Corresponds to SEQ ID NO:12, nucleotides 3686..>4913
      Product="4hworf3i"
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caa gaa aat gat gaa agg aat caa act ggt gaa tca ggt gtt aaa cct 96
 Gln Glu Asn Asp Glu Arg Asn Gln Thr Gly Glu Ser Gly Val Lys Pro
 20 25 30

gaa gta cca aac cag caa agt att caa gat ata ggt cag ggt gta gta 144
 Glu Val Pro Asn Gln Gln Ser Ile Gln Asp Ile Gly Gln Gly Val Val
 35 40 45

gaa ggg gca aca gat gct agt gat atg agt ggt gtt gga aga tgt gct 192
 Glu Gly Ala Thr Asp Ala Ser Asp Met Ser Gly Val Gly Arg Cys Ala
 50 55 60

ttt tct gtg act ata gag att gaa tca tct tca tca aca tct cag cca 240
 Phe Ser Val Thr Ile Glu Ile Glu Ser Ser Ser Ser Thr Ser Gln Pro
 65 70 75 80

agt aqt aqt ctt qaa aat ata tat atq agg caq qqt qct agg cca aaa 288

Ser Ser Ser Leu Glu Asn Ile Tyr Met Arg Gln Gly Ala Arg Pro Lys
 85 90 95

 act agg act caa agt aaa gtt gca cag cag agt aca gga caa ttt cag 336
 Thr Arg Thr Gln Ser Lys Val Ala Gln Gln Ser Thr Gly Gln Phe Gln
 100 105 110

 agt ata ggg tca cag agt agt ttg cct cct gta ttt gta aaa cgt atg 384
 Ser Ile Gly Ser Gln Ser Ser Leu Pro Pro Val Phe Val Lys Arg Met
 115 120 125

 gct gat gta tct ttg gaa aag gca gaa tgt gat aca tat ata tgt ggg 432
 Ala Asp Val Ser Leu Glu Lys Ala Glu Cys Asp Thr Tyr Ile Cys Gly
 130 135 140

 act aaa agg cgt agc gat caa agc aca agg tca agg gag gac tta cct 480
 Thr Lys Arg Arg Ser Asp Gln Ser Thr Arg Ser Arg Glu Asp Leu Pro
 145 150 155 160

 tct agg ttt gca aaa tgt gca tct gat ata ttt tta aca aag cca caa 528
 Ser Arg Phe Ala Lys Cys Ala Ser Asp Ile Phe Leu Thr Lys Pro Gln
 165 170 175

 aat aat gat cta gat att cat gat act gat aaa gag aaa tta ata cat 576
 Asn Asn Asp Leu Asp Ile His Asp Thr Asp Lys Glu Lys Leu Ile His
 180 185 190

 tca tta gaa gaa tta gat gtt gct ctg cct act gag tct gga ggt gat 624
 Ser Leu Glu Glu Leu Asp Val Ala Leu Pro Thr Glu Ser Gly Gly Asp
 195 200 205

 cat aat gtt tta tct gat gtc gta tat aaa aaa tgt gta tcc tta caa 672
 His Asn Val Leu Ser Asp Val Val Tyr Lys Lys Cys Val Ser Leu Gln
 210 215 220

 caa aaa tgt ggc agt ttt aga cag ttt agt aat tct tgt cta gca aga 720
 Gln Lys Cys Gly Ser Phe Arg Gln Phe Ser Asn Ser Cys Leu Ala Arg
 225 230 235 240

 tta aga ggt atg cat atg gga tat ctt aat ttt ttt atg aaa cga ttg 768
 Leu Arg Gly Met His Met Gly Tyr Leu Asn Phe Phe Met Lys Arg Leu
 245 250 255

 ttt atg gct caa ggt aac aca tta gtt atg cgt ggg gag tac ttg cag 816
 Phe Met Ala Gln Gly Asn Thr Leu Val Met Arg Gly Glu Tyr Leu Gln
 260 265 270

 atg tta tca aat atc act aaa cat tct gac gag gct gtt gtt ctt gtg 864
 Met Leu Ser Asn Ile Thr Lys His Ser Asp Glu Ala Val Val Leu Val
 275 280 285

 aag tta aat ctt atg tca caa tat ttg ctt gca ttt ggt gcg tat cag 912
 Lys Leu Asn Leu Met Ser Gln Tyr Leu Leu Ala Phe Gly Ala Tyr Gln
 290 295 300

gta agc cgg tca atg tta aca cag aag ctt agt aat tct gat ttt tat		960	
Val Ser Arg Ser Met Leu Thr Gln Lys Leu Ser Asn Ser Asp Phe Tyr			
305	310	315	320
gca att gat att ttg tta tta gaa tta ata ttg gtt tcg tac aag gag		1008	
Ala Ile Asp Ile Leu Leu Glu Leu Ile Leu Val Ser Tyr Lys Glu			
325	330	335	
aga gtg aat ctt tat tgt gct caa aga gaa gtt ctt agg atg tat gct		1056	
Arg Val Asn Leu Tyr Cys Ala Gln Arg Glu Val Leu Arg Met Tyr Ala			
340	345	350	
ata atg gat tat aat tct ggt tat aat cct aat tgt agt aat ata aag		1104	
Ile Met Asp Tyr Asn Ser Gly Tyr Asn Pro Asn Cys Ser Asn Ile Lys			
355	360	365	
ttt tgt tat gta atg gtg caa tta ttc cgt gat tta tta tct gca aga		1152	
Phe Cys Tyr Val Met Val Gln Leu Phe Arg Asp Leu Leu Ser Ala Arg			
370	375	380	
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Gln Ser Met Val Leu Gly Asp Leu Asp Leu Gln Leu Val Asn Leu Leu			
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)			
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Glu Val Pro Asn Gln Gln Ser Ile Gln Asp Ile Gly Gln Gly Val Val			
35	40	45	
Glu Gly Ala Thr Asp Ala Ser Asp Met Ser Gly Val Gly Arg Cys Ala			
50	55	60	
Phe Ser Val Thr Ile Glu Ile Glu Ser Ser Ser Ser Thr Ser Gln Pro			
65	70	75	80

Ser Ser Ser Leu Glu Asn Ile Tyr Met Arg Gln Gly Ala Arg Pro Lys
85 90 95

Thr Arg Thr Gln Ser Lys Val Ala Gln Gln Ser Thr Gly Gln Phe Gln
100 105 110

Ser Ile Gly Ser Gln Ser Ser Leu Pro Pro Val Phe Val Lys Arg Met
115 120 125

Ala Asp Val Ser Leu Glu Lys Ala Glu Cys Asp Thr Tyr Ile Cys Gly
130 135 140

Thr Lys Arg Arg Ser Asp Gln Ser Thr Arg Ser Arg Glu Asp Leu Pro
145 150 155 160

Ser Arg Phe Ala Lys Cys Ala Ser Asp Ile Phe Leu Thr Lys Pro Gln
165 170 175

Asn Asn Asp Leu Asp Ile His Asp Thr Asp Lys Glu Lys Leu Ile His
180 185 190

Ser Leu Glu Glu Leu Asp Val Ala Leu Pro Thr Glu Ser Gly Gly Asp
195 200 205

His Asn Val Leu Ser Asp Val Val Tyr Lys Lys Cys Val Ser Leu Gln
210 215 220

Gln Lys Cys Gly Ser Phe Arg Gln Phe Ser Asn Ser Cys Leu Ala Arg
225 230 235 240

Leu Arg Gly Met His Met Gly Tyr Leu Asn Phe Phe Met Lys Arg Leu
245 250 255

Phe Met Ala Gln Gly Asn Thr Leu Val Met Arg Gly Glu Tyr Leu Gln
260 265 270

Met Leu Ser Asn Ile Thr Lys His Ser Asp Glu Ala Val Val Leu Val
275 280 285

Lys Leu Asn Leu Met Ser Gln Tyr Leu Leu Ala Phe Gly Ala Tyr Gln
290 295 300

Val Ser Arg Ser Met Leu Thr Gln Lys Leu Ser Asn Ser Asp Phe Tyr
 305 310 315 320

Ala Ile Asp Ile Leu Leu Glu Leu Ile Leu Val Ser Tyr Lys Glu
 325 330 335

Arg Val Asn Leu Tyr Cys Ala Gln Arg Glu Val Leu Arg Met Tyr Ala
 340 345 350

Ile Met Asp Tyr Asn Ser Gly Tyr Asn Pro Asn Cys Ser Asn Ile Lys
 355 360 365

Phe Cys Tyr Val Met Val Gln Leu Phe Arg Asp Leu Leu Ser Ala Arg
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Ile Ile Ser Val Ser Ile Gln Ile Asp
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<210> 19
<211> 6190
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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aagtttttat ttacaaaaga cttgtataaa atcgcaatac aaaatattga atacatgaac	180
aaaattgaag aacccaaacat taattgataa agtataattgt tattatatac ctacaactat	240
tatttgtatc atatgacaat ttcttattaa ataatagtaa aaataatttt tatacagcaa	300
gatttgatac ttaccataat aaagtatcac aacaaaacca tataaaataa gaaagttagta	360
cacacattat aaaaataacg ttaatcaccc attgcaatga cataataagt tacatggta	420
cactttgat acttataata gttataataa aaagtagttat aataaaacca aaaccatata	480
aaataagaaa gtaccacaca ttatagaaat aataccggtc acccattgca atgacataat	540
aagttacatg ggtacacttt tgacacttat aatagttaat aataaaagta gtataacaaa	600

actaaaacca tataaaataa gaaagtacca cacattacag aaacaatact ggtcacacat	660
tgcaatgaca taataagtta catgggtaca ctttgatac ttataatagt taataataaa	720
agtagtataa taaaacccaaa accatataaa ataagaagt accacacatt acagaaacaa	780
tactggtcac ccattgcaat gacataataa gttacatggg tacactttt atacttataa	840
tagttaataa taaaagtagt ataataaaac caaaaccata taaaataaga aagtaccaca	900
cattacagaa ataataccgg tcacccattg caatagcata ataagttata ttaatacacg	960
ttcaattatt tatacattga gaaatccata aactcactt gtttagcata tattacatac	1020
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ctttgcttt ttagataga tagtacacac ggagttgaag ctgagacctt agcaaatgtg	6120
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<210> 20
 <211> 975
 <212> DNA
 <213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
 <221> misc_feature
 <222> (1)..(975)
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 Hypothetical ribonucleoside reductase, beta chain
 Product="6hworf1"

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caaagggttc ttatggcg tttatataagg ctctaaattt aactgttatta gccttctatt	180
tgcaatataat cttatataatt cttaacctc ctgagcagac aaaccttcaa catcaccaca	240
agcaaatgcc aaattaataa actcatcttc taaagttaca ataacactac atgcttcata	300
caattccctt ttaagatcat catccatat ttcataattt tcttgaataa aagtattaaa	360
taatctaatt atcgactcag tatgtatgt ttcatacgac acagaccaag caataatttg	420
tcccatgcct ttcattttcc caaaacgttg aaaatttagt aaaattgcaa atgaagcaa	480

caattgtaaa ccttctgtaa aggcaccaaa aactgctaaa gttttgcta catgccttt	540
gtcattctt ctacactctt caaacggtg catgtagtca tatttcttt tcataacctc	600
aaatttcaaa aacgcctgat actctatttc tggcatccca atagtatcca ataagtaaga	660
ataaggcagca atatgtatacg tttccatatt tgaaaatgca gataacatca tacatatttc	720
cgttggctta aatatatttg aataatgttt catataacag ttattaactt cgatatcagc	780
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<210> 21
<211> 1947
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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<223> Corresponds to SEQ ID NO:19, nucleotides 3126..5072
Product = "6hworf2"

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1 5 10 15	

ata ttt gca gac tct cag att cac ata aca gag gaa caa tta aaa ata	96
Ile Phe Ala Asp Ser Gln Ile His Ile Thr Glu Glu Gln Leu Lys Ile	
20 25 30	

tat ata aag aat ctt ata gat aac tta tat gta tat aac cta cta gat	144
Tyr Ile Lys Asn Leu Ile Asp Asn Leu Tyr Val Tyr Asn Leu Leu Asp	
35 40 45	

cct gga aat gct ata cca ttg tct att ata gca atg cta ggt cta cat	192
Pro Gly Asn Ala Ile Pro Leu Ser Ile Ile Ala Met Leu Gly Leu His	
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tca gat ttt cat tca ttt aaa aaa gca gta cta gat act ctt tct gga	240
Ser Asp Phe His Ser Phe Lys Lys Ala Val Leu Asp Thr Leu Ser Gly	
65 70 75 80	

tac aaa aat tct gtc cat agt ttt ctt gca cag tct aca ata att gac	288
Tyr Lys Asn Ser Val His Ser Phe Leu Ala Gln Ser Thr Ile Ile Asp	
85 90 95	

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100 105 110	
cca cct ctt ttg gat aaa aga act tca gaa gat atg tgg aat gat att Pro Pro Leu Leu Asp Lys Arg Thr Ser Glu Asp Met Trp Asn Asp Ile	384
115 120 125	
aaa gaa tta cac ata tta tat cac caa tat ata att aac gta tct gta Lys Glu Leu His Ile Leu Tyr His Gln Tyr Ile Ile Asn Val Ser Val	432
130 135 140	
gat aaa agt act aat gct ata agc aat aca gta aat gct cca ggc acc Asp Lys Ser Thr Asn Ala Ile Ser Asn Thr Val Asn Ala Pro Gly Thr	480
145 150 155 160	
aaa aca tgt tct att aag ata tcg tat act aat cca tta aga cag cat Lys Thr Cys Ser Ile Lys Ile Ser Tyr Thr Asn Pro Leu Arg Gln His	528
165 170 175	
gta cac tat ttt aca tta aaa aca ctt att gaa tat tac aac act caa Val His Tyr Phe Thr Leu Lys Thr Leu Ile Glu Tyr Tyr Asn Thr Gln	576
180 185 190	
caa aca tca tta aca ggt cac aga tca att gat gat caa caa gaa gct Gln Thr Ser Leu Thr Gly His Arg Ser Ile Asp Asp Gln Gln Glu Ala	624
195 200 205	
gct gtt act ttg ttt aaa gaa aca tta gaa gaa aaa ttt tgc aaa gga Ala Val Thr Leu Phe Lys Glu Thr Leu Glu Glu Lys Phe Cys Lys Gly	672
210 215 220	
tta aaa aat aaa ata ttt ttt aat tat gca caa tat tta aaa agt cta Leu Lys Asn Lys Ile Phe Phe Asn Tyr Ala Gln Tyr Leu Lys Ser Leu	720
225 230 235 240	
ttt act atc gta aca tca aat cca aaa gta gac tat acc ctt cca caa Phe Thr Ile Val Thr Ser Asn Pro Lys Val Asp Tyr Thr Leu Pro Gln	768
245 250 255	
aat ata tat aga tat tgt gaa aca aga aga atg gta att tca aaa ata Asn Ile Tyr Arg Tyr Cys Glu Thr Arg Arg Met Val Ile Ser Lys Ile	816
260 265 270	
aca cat gat ata att cct ata tca gat cca gga act gat ata cgt att Thr His Asp Ile Ile Pro Ile Ser Asp Pro Gly Thr Asp Ile Arg Ile	864
275 280 285	
tat tgt gat ata cca gag tat gta acc gta tta tca gaa aca agt aac Tyr Cys Asp Ile Pro Glu Tyr Val Thr Val Leu Ser Glu Thr Ser Asn	912
290 295 300	
att act ata tac ggg aaa gaa gta ctt ggt aaa gtt tat agc ata tat Ile Thr Ile Tyr Gly Lys Glu Val Leu Gly Lys Val Tyr Ser Ile Tyr	960

305	310	315	320	
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ata ctt aat cgg aaa cat aca ata cct agt ata ttt gaa att aac aac Ile Leu Asn Arg Lys His Thr Ile Pro Ser Ile Phe Glu Ile Asn Asn 355 360 365				1104
cat aac aca tac tta tca ctt aaa tat aat tct ata tta aca aaa ata His Asn Thr Tyr Leu Ser Leu Lys Tyr Asn Ser Ile Leu Thr Lys Ile 370 375 380				1152
aca agc agc tct gta ggt tcc gta aat gaa gaa aaa aaa tca caa atc Thr Ser Ser Val Gly Ser Val Asn Glu Glu Lys Lys Ser Gln Ile 385 390 395 400				1200
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aca gct act gtc ata tca tta gat tta aaa gat cat cca tta cct att Thr Ala Thr Val Ile Ser Leu Asp Leu Lys Asp His Pro Leu Pro Ile 435 440 445				1344
act aat aat aat act ata cct aat ata tta agc cta aca gac aat cac Thr Asn Asn Asn Thr Ile Pro Asn Ile Leu Ser Leu Thr Asp Asn His 450 455 460				1392
gca aca gat tca gaa tta cca agt gag ttt ttt agt aac aat gtt aac Ala Thr Asp Ser Glu Leu Pro Ser Glu Phe Phe Ser Asn Asn Val Asn 465 470 475 480				1440
cca aaa agt gct gga att acg aga ata aaa aat aca att att att gag Pro Lys Ser Ala Gly Ile Thr Arg Ile Lys Asn Thr Ile Ile Glu 485 490 495				1488
aaa tta act cct aca ata gga aga tat atg aat gtt gcc aca aaa aat Lys Leu Thr Pro Thr Ile Gly Arg Tyr Met Asn Val Ala Thr Lys Asn 500 505 510				1536
gga aca gta tta gat aaa tat ggg atc aca gaa gta att att caa agt Gly Thr Val Leu Asp Lys Tyr Gly Ile Thr Glu Val Ile Ile Gln Ser 515 520 525				1584
acc aga aac ttt gta ata tta cta cat gat gca aat gtt act ata				1632

Thr Arg Asn Phe Val Ile Leu Leu Leu His Asp Ala Asn Val Thr Ile			
530	535	540	
gaa tgt cca ttt tct gga gaa ata ttt aca aat aca ggt aat att aca			1680
Glu Cys Pro Phe Ser Gly Glu Ile Phe Thr Asn Thr Gly Asn Ile Thr			
545	550	555	560
gtt att ggc cca gta act cac aat tct aaa ctt att tca aac ttt ggt			1728
Val Ile Gly Pro Val Thr His Asn Ser Lys Leu Ile Ser Asn Phe Gly			
565	570	575	
tca gtt tat gtt ggt aat ata tct cat cgg tca aat gca tta gca ata			1776
Ser Val Tyr Val Gly Asn Ile Ser His Arg Ser Asn Ala Leu Ala Ile			
580	585	590	
gat aac agc cgt att gta tct tca ctt ggg cat gtc aca att tat ggc			1824
Asp Asn Ser Arg Ile Val Ser Ser Leu Gly His Val Thr Ile Tyr Gly			
595	600	605	
aaa gtt agt aaa tcc aat att act act tct aca tca gat gca ata tca			1872
Lys Val Ser Lys Ser Asn Ile Thr Thr Ser Thr Ser Asp Ala Ile Ser			
610	615	620	
ata cat aac tca ata tca tgg ttt gat aaa cta act tct tgt aac acc			1920
Ile His Asn Ser Ile Ser Trp Phe Asp Lys Leu Thr Ser Cys Asn Thr			
625	630	635	640
aaa act tta gca tct cgc aaa aca taa			1947
Lys Thr Leu Ala Ser Arg Lys Thr			
645			
<210> 22			
<211> 648			
<212> PRT			
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)			
<400> 22			
Met Leu Gly Asn Ser Gln Glu Ser Ser Ile Ser Ser Glu Thr Leu Glu			
1	5	10	15
Ile Phe Ala Asp Ser Gln Ile His Ile Thr Glu Glu Gln Leu Lys Ile			
20	25	30	
Tyr Ile Lys Asn Leu Ile Asp Asn Leu Tyr Val Tyr Asn Leu Leu Asp			
35	40	45	
Pro Gly Asn Ala Ile Pro Leu Ser Ile Ile Ala Met Leu Gly Leu His			
50	55	60	

Ser Asp Phe His Ser Phe Lys Lys Ala Val Leu Asp Thr Leu Ser Gly
65 70 75 80

Tyr Lys Asn Ser Val His Ser Phe Leu Ala Gln Ser Thr Ile Ile Asp
85 90 95

Arg Ser Glu Ser Leu Arg Ala Glu Pro Asn His Cys Leu Tyr Ser Leu
100 105 110

Pro Pro Leu Leu Asp Lys Arg Thr Ser Glu Asp Met Trp Asn Asp Ile
115 120 125

Lys Glu Leu His Ile Leu Tyr His Gln Tyr Ile Ile Asn Val Ser Val
130 135 140

Asp Lys Ser Thr Asn Ala Ile Ser Asn Thr Val Asn Ala Pro Gly Thr
145 150 155 160

Lys Thr Cys Ser Ile Lys Ile Ser Tyr Thr Asn Pro Leu Arg Gln His
165 170 175

Val His Tyr Phe Thr Leu Lys Thr Leu Ile Glu Tyr Tyr Asn Thr Gln
180 185 190

Gln Thr Ser Leu Thr Gly His Arg Ser Ile Asp Asp Gln Gln Glu Ala
195 200 205

Ala Val Thr Leu Phe Lys Glu Thr Leu Glu Glu Lys Phe Cys Lys Gly
210 215 220

Leu Lys Asn Lys Ile Phe Phe Asn Tyr Ala Gln Tyr Leu Lys Ser Leu
225 230 235 240

Phe Thr Ile Val Thr Ser Asn Pro Lys Val Asp Tyr Thr Leu Pro Gln
245 250 255

Asn Ile Tyr Arg Tyr Cys Glu Thr Arg Arg Met Val Ile Ser Lys Ile
260 265 270

Thr His Asp Ile Ile Pro Ile Ser Asp Pro Gly Thr Asp Ile Arg Ile
275 280 285

Tyr Cys Asp Ile Pro Glu Tyr Val Thr Val Leu Ser Glu Thr Ser Asn
290 295 300

Ile Thr Ile Tyr Gly Lys Glu Val Leu Gly Lys Val Tyr Ser Ile Tyr
305 310 315 320

Gly Thr Ile Ile Ile Lys Asn Asn Met Pro His Asn Glu Arg Glu Ile
325 330 335

Ser Ser Arg Ile Cys Ser Leu Phe Gly Arg Val Ile Ile Asn Gly Arg
340 345 350

Ile Leu Asn Arg Lys His Thr Ile Pro Ser Ile Phe Glu Ile Asn Asn
355 360 365

His Asn Thr Tyr Leu Ser Leu Lys Tyr Asn Ser Ile Leu Thr Lys Ile
370 375 380

Thr Ser Ser Ser Val Gly Ser Val Asn Glu Glu Lys Lys Ser Gln Ile
385 390 395 400

Phe Glu Ile Ser Arg Asp Thr Ile Leu Asn Ser Thr Asn Tyr Gln Arg
405 410 415

Asn Ile Ser Asn Leu Lys Ile Glu Leu His Asn Pro Asp Glu Gln Leu
420 425 430

Thr Ala Thr Val Ile Ser Leu Asp Leu Lys Asp His Pro Leu Pro Ile
435 440 445

Thr Asn Asn Asn Thr Ile Pro Asn Ile Leu Ser Leu Thr Asp Asn His
450 455 460

Ala Thr Asp Ser Glu Leu Pro Ser Glu Phe Phe Ser Asn Asn Val Asn
465 470 475 480

Pro Lys Ser Ala Gly Ile Thr Arg Ile Lys Asn Thr Ile Ile Glu
485 490 495

Lys Leu Thr Pro Thr Ile Gly Arg Tyr Met Asn Val Ala Thr Lys Asn
500 505 510

Gly Thr Val Leu Asp Lys Tyr Gly Ile Thr Glu Val Ile Ile Gln Ser
 515 520 525

Thr Arg Asn Phe Val Ile Leu Leu His Asp Ala Asn Val Thr Ile
 530 535 540

Glu Cys Pro Phe Ser Gly Glu Ile Phe Thr Asn Thr Gly Asn Ile Thr
 545 550 555 560

Val Ile Gly Pro Val Thr His Asn Ser Lys Leu Ile Ser Asn Phe Gly
 565 570 575

Ser Val Tyr Val Gly Asn Ile Ser His Arg Ser Asn Ala Leu Ala Ile
 580 585 590

Asp Asn Ser Arg Ile Val Ser Ser Leu Gly His Val Thr Ile Tyr Gly
 595 600 605

Lys Val Ser Lys Ser Asn Ile Thr Thr Ser Thr Ser Asp Ala Ile Ser
 610 615 620

Ile His Asn Ser Ile Ser Trp Phe Asp Lys Leu Thr Ser Cys Asn Thr
 625 630 635 640

Lys Thr Leu Ala Ser Arg Lys Thr
 645

<210> 23
<211> 2778
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 23			
gatctacaaa taaaagtca	gc aaaaccacta actataagcc ttcttg	ggc atttacaata	60
atatctacat ctatatatat	agctttcggt aaatgagctt	ttaatgactt tttgttacca	120
ccactaaatg ttatagatgc	atttgatgaa ctataccat	tcatagaagg agctgttagga	180
aatgaaatat aatttttatt	tgtaatgtaa ctcacatatt	tacaaagatc atttatttg	240
ccactaccaa aagatactaa	aatatcagca tcttgtgatt	tttctgtaat taattctact	300
aacgtttgag atgcacaata	ttttgcagg attataaaat	ttttaaaagt attaaataca	360

actttatcca ataaaggcgc agtatttaca tcagctacta taaaaggcaca attaccatgc 420
tgcctaataa tatcacatat gttagaactg atttttctat caatatatat attatctata 480
atattaacta ctgaacttaa ttccataaaaaa ttttttatcaa gcaaaaacttg ctttagaaaac 540
ttatcataca taataaaaaa acaagctata tgctattatt gtaacttaat agctaagttt 600
aaaaaatctct tatagtaaaag tataccaata aaactaaatc ttggaaaaaa ctttctcaaa 660
tttaaaaat taatttttt tttacaatac gatactagaa cacacacata tattagttaa 720
ctacaaatac cagtgtactg ctaattcaac atataagtca ttgcttataa taacattatt 780
aattaaaaaa taactattct agccagtgtt catcacacta tgtcattta cagtagatca 840
caacttaaag aaacaaaata ctataaaat aacacattaa aagcatatca ataatactta 900
ataataacca tcaatgttta taatttatgt aaaataaaaa acctttattc ttaatcatta 960
cactttatgt atatattaca aattttgaa caataataaa ttggactatc aagaatagtt 1020
gtcattttaa gtttatcaca acataggaaa ttcttatatcc ctattataag taacatatat 1080
atttaaataa tacaatcaac aaataaacac actacaactg ataaggttac acctactata 1140
aacatataga taaataaaaa ttcaacataa ctatcacca tataagacaa atactgtttt 1200
tttgaatata ggaacattaa taacctacta taaatgttc taactttaag tatagtacaa 1260
aacaataac tcattttaa tttatattaa atatatatat tttaactaca taaattaatt 1320
accattataa agaaatataat atacttgaga attatcaaaa tatttatctt actatctaa 1380
ttaatatagt tgccttatct acataactgc aattgactaa cttatcacag ttgatatgat 1440
taagaatagc aaaattttac tttatatgtg tttatatgga gactagatgt cagcaaattcc 1500
cttagatcag tttaggattt ccactatatt caagctaccc gatattggcg aatataat 1560
tgattttact aatgcctcat tatttatggc attatccaca tttttatct ctttgtctg 1620
ctatgttggc ttaaggaaag aaagtgttat tccgaatcca ttacaatcaa taatagaaat 1680
tatttatgtat tttattgttt ctacaataga aagtaatgta ggtaaggaag gattacaata 1740
cgtaccatta gttttacaa tatttacatt cattctagta tgtaatctt taggtatatt 1800
accattaggg ttcaactgtaa caagtcatac tgcaatcata tttgcaatata caatgattgt 1860
attcataagt gtaacattca taggatttaa acaccaagga actcatttcc ttccatatt 1920
gttaccacaa ggcacacacaa tgtggtagc acctatgatg gtcttaatttgc 1980

ctattgcgca cgccctgtaa gcctatcaat acgactcgct gctaataatga tagctggcca 2040
 tactattatc aaggtagttag caggattcggtataaaatatg aatatatttt taacaccctt 2100
 acctatagca ttcattataa tacttattgg gtttgaataa ttcgttgcaa tcctacaggc 2160
 atacattttt acagtaactca cttgtgtgtatctatcagat gcagtaataa agcactaaat 2220
 tttagcgatt gacttcgtat aatgatctac ttataattct tctagctttt tataaaggta 2280
 agagtgtatg gattcttaa agtttattgc tgtagggta agtgttttg gtatgggtgc 2340
 ttctgcttta ggggttgcaa atatatttc tactatgcta aatggattag cacgtaatcc 2400
 tgaaacagaa gataaaactaa aaaaatatgt ttatactggt gctgcttttag ttgaagcaat 2460
 gggtttattt tcttccttat tagccctatt actaattttt gtagcctaattttagatttt 2520
 ggacacaata ccacagttag atatacttc ttatccttct cagttttttt ggttttttt 2580
 atcttttagt gttttgtaca ttataattag taaaaatgtg ctgccaaaga ttgaaaatat 2640
 agtaagaaag aggtataata ttataagatg ttctattgtatctgttaagg gtgatttaag 2700
 ccatgcgcag caagagttag ataaacagct gctaaagctt actgcagttac aagcagaagt 2760
 agatagaatt atacgatc 2778

<210> 24
 <211> 551
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(551)
 <223> Complement to SEQ ID NO:23, nucleotides <1..551
 Hypothetical AraM protein
 Product = "9hworfli"

<400> 24
 gatctacaaa taaagtcagc aaaaccacta actataagcc ttcttggcgc atttacaata 60
 atatctacat ctatataat agcttcggtaatgagctt ttaatgactt tttgttacca 120
 ccactaaatg ttatagatgc atttgcataa ctataccat tcatagaagg agctgttagga 180
 aatgaaatat aatttttatt tgtaatgtaa ctcacatatt tacaaagatc atttattgtg 240
 ccactaccaa aagataactaa aatatcagca tcttgcattttctgtat taattctact 300
 aacgtttgag atgcacaata tttttgcagg attataaaat ttttaaaagt attaaataca 360

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actttat tta ataaaggcagc agtatttaca tcagctacta taaaaggcaca attaccatgc 420  
tgcctaataa tatcacatat gttagaactg atttttctat caatatatat attatctata 480  
atattaacta ctgaacttaa ttcataaaaaa ttttatcaa gcaaaaacttg cttagaaac 540  
ttatcataca t 551
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<210> 25
<211> 732
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(732)
<223> Corresponds to SEQ ID NO:23, nucleotides 1487..2218
Hypothetical ATP synthase A chain
Product = "9hworf2"

```

<400> 25
atg tca gca aat ccc tta gat cag ttt agg att tcc act ata ttc aag      48
Met Ser Ala Asn Pro Leu Asp Gln Phe Arg Ile Ser Thr Ile Phe Lys
1          5                  10                   15

```

ctt cct gat att ggc gaa tat aat att gat ttt act aat gcc tca tta 96
 Leu Pro Asp Ile Gly Glu Tyr Asn Ile Asp Phe Thr Asn Ala Ser Leu
 20 25 30

ttt atg gta tta tcc aca ttt tta atc tcc ttg tct tgc tat gtt gga
 Phe Met Val Leu Ser Thr Phe Leu Ile Ser Leu Ser Cys Tyr Val Gly

 35 40 45

```
tta agg aaa gaa agt gtt att ccg aat cca tta caa tca ata ata gaa      192
Leu Arg Lys Glu Ser Val Ile Pro Asn Pro Leu Gln Ser Ile Ile Glu
      50          55          60
```

att att tat gat ttt att gtt tct aca ata gaa agt aat gta ggt aag 240
Ile Ile Tyr Asp Phe Ile Val Ser Thr Ile Glu Ser Asn Val Gly Lys
65 70 75 80

gaa gga tta caa tac gta cca tta gtt ttt aca ata ttt aca ttc att 288
 Glu Gly Leu Gln Tyr Val Pro Leu Val Phe Thr Ile Phe Thr Phe Ile
 85 90 95

ctt gta tgt aat ctc tta ggt ata tta cca tta ggg ttc act gta aca 336
 Leu Val Cys Asn Leu Leu Gly Ile Leu Pro Leu Gly Phe Thr Val Thr
 100 105 110

agt cat att gca gta aca ttt gca ata tca atg att gta ttc ata agt 384
 Ser His Ile Ala Val Thr Phe Ala Ile Ser Met Ile Val Phe Ile Ser
 115 120 125

gta aca ttc ata gga ttt aaa cac caa gga act cat ttc ctt cat ata		432
Val Thr Phe Ile Gly Phe Lys His Gln Gly Thr His Phe Leu His Ile		
130	135	140
ttg tta cca caa ggc aca cca atg tgg tta gca cct atg atg gtc tta		480
Leu Leu Pro Gln Gly Thr Pro Met Trp Leu Ala Pro Met Met Val Leu		
145	150	155
160		
att gaa tta ttt gcc tat tgc gca cgc cct gta agc cta tca ata cga		528
Ile Glu Leu Phe Ala Tyr Cys Ala Arg Pro Val Ser Leu Ser Ile Arg		
165	170	175
ctc gct gct aat atg ata gct ggc cat act att atc aag gtt ata gca		576
Leu Ala Ala Asn Met Ile Ala Gly His Thr Ile Ile Lys Val Ile Ala		
180	185	190
gga ttc gtt ata aat atg aat ata ttt tta aca cct tta cct ata gca		624
Gly Phe Val Ile Asn Met Asn Ile Phe Leu Thr Pro Leu Pro Ile Ala		
195	200	205
ttc att ata ata ctt att ggg ttt gaa ata ttc gtt gca atc tta cag		672
Phe Ile Ile Leu Ile Gly Phe Glu Ile Phe Val Ala Ile Leu Gln		
210	215	220
gca tac att ttt aca gta ctc act tgt gtg tac tta tca gat gca gta		720
Ala Tyr Ile Phe Thr Val Leu Thr Cys Val Tyr Leu Ser Asp Ala Val		
225	230	235
240		
aat aag cac taa		732
Asn Lys His		

<210> 26
<211> 243
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
<400> 26

Met Ser Ala Asn Pro Leu Asp Gln Phe Arg Ile Ser Thr Ile Phe Lys
1 5 10 15

Leu Pro Asp Ile Gly Glu Tyr Asn Ile Asp Phe Thr Asn Ala Ser Leu
20 25 30

Phe Met Val Leu Ser Thr Phe Leu Ile Ser Leu Ser Cys Tyr Val Gly
35 40 45

Leu Arg Lys Glu Ser Val Ile Pro Asn Pro Leu Gln Ser Ile Ile Glu
50 55 60

Ile Ile Tyr Asp Phe Ile Val Ser Thr Ile Glu Ser Asn Val Gly Lys
65 70 75 80

Glu Gly Leu Gln Tyr Val Pro Leu Val Phe Thr Ile Phe Thr Phe Ile
85 90 95

Leu Val Cys Asn Leu Leu Gly Ile Leu Pro Leu Gly Phe Thr Val Thr
100 105 110

Ser His Ile Ala Val Thr Phe Ala Ile Ser Met Ile Val Phe Ile Ser
115 120 125

Val Thr Phe Ile Gly Phe Lys His Gln Gly Thr His Phe Leu His Ile
130 135 140

Leu Leu Pro Gln Gly Thr Pro Met Trp Leu Ala Pro Met Met Val Leu
145 150 155 160

Ile Glu Leu Phe Ala Tyr Cys Ala Arg Pro Val Ser Leu Ser Ile Arg
165 170 175

Leu Ala Ala Asn Met Ile Ala Gly His Thr Ile Ile Lys Val Ile Ala
180 185 190

Gly Phe Val Ile Asn Met Asn Ile Phe Leu Thr Pro Leu Pro Ile Ala
195 200 205

Phe Ile Ile Ile Leu Ile Gly Phe Glu Ile Phe Val Ala Ile Leu Gln
210 215 220

Ala Tyr Ile Phe Thr Val Leu Thr Cys Val Tyr Leu Ser Asp Ala Val
225 230 235 240

Asn Lys His

<210> 27
<211> 222
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS
 <222> (1)..(222)
 <223> Corresponds to SEQ ID NO:23, nucleotides 2288..2509
 Hypothetical ATP synthase C chain
 Product = "9hworf3"

<400> 27
 atg gat tct tta aag ttt att gct gta ggg tta agt gtt ttt ggt atg 48
 Met Asp Ser Leu Lys Phe Ile Ala Val Gly Leu Ser Val Phe Gly Met
 1 5 10 15

gtt gct tct gct tta ggg gtt gca aat ata ttt tct act atg cta aat 96
 Val Ala Ser Ala Leu Gly Val Ala Asn Ile Phe Ser Thr Met Leu Asn
 20 25 30

gga tta gca cgt aat cct gaa aca gaa gat aaa cta aaa aaa tat gtt 144
 Gly Leu Ala Arg Asn Pro Glu Thr Glu Asp Lys Leu Lys Lys Tyr Val
 35 40 45

tat act ggt gct gct tta gtt gaa gca atg ggt tta ttt tct ttc cta 192
 Tyr Thr Gly Ala Ala Leu Val Glu Ala Met Gly Leu Phe Ser Phe Leu
 50 55 60

tta gcc cta tta cta att ttt gta gcc taa 222
 Leu Ala Leu Leu Ile Phe Val Ala
 65 70

<210> 28
 <211> 73
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 28
 Met Asp Ser Leu Lys Phe Ile Ala Val Gly Leu Ser Val Phe Gly Met
 1 5 10 15

Val Ala Ser Ala Leu Gly Val Ala Asn Ile Phe Ser Thr Met Leu Asn
 20 25 30

Gly Leu Ala Arg Asn Pro Glu Thr Glu Asp Lys Leu Lys Lys Tyr Val
 35 40 45

Tyr Thr Gly Ala Ala Leu Val Glu Ala Met Gly Leu Phe Ser Phe Leu
 50 55 60

Leu Ala Leu Leu Ile Phe Val Ala
 65 70

<210> 29
<211> 261
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)..(261)
<223> Corresponds to SEQ ID NO:23, nucleotides 2519..>2778
Hypothetical ATP synthase B chain
Product="9hworf4i"

<220>
<221> misc_feature
<222> (261)..(261)
<223> n = a, c, g, or t

<400> 29		
atg gac aca ata cca cag tta gat ata tct tct tat cct tct cag ttt		48
Met Asp Thr Ile Pro Gln Leu Asp Ile Ser Ser Tyr Pro Ser Gln Phe		
1 5 10 15		
ttt tgg ttt ttt tta tct ttt agt gtt ttg tac att ata att att agt aaa		96
Phe Trp Phe Phe Leu Ser Phe Ser Val Leu Tyr Ile Ile Ser Lys		
20 25 30		
aat gtg ctg cca aag att gaa aat ata gta aga aag agg tat aat att		144
Asn Val Leu Pro Lys Ile Glu Asn Ile Val Arg Lys Arg Tyr Asn Ile		
35 40 45		
ata aga tgt tct att gat tct gtt aag ggt gat tta agc cat gcg cag		192
Ile Arg Cys Ser Ile Asp Ser Val Lys Gly Asp Leu Ser His Ala Gln		
50 55 60		
caa gag tta gat aaa cag ctg cta aag ctt act gca gta caa gca gaa		240
Gln Glu Leu Asp Lys Gln Leu Leu Lys Leu Thr Ala Val Gln Ala Glu		
65 70 75 80		
gta gat aga att ata cga tcn		261
Val Asp Arg Ile Ile Arg Xaa		
85		

<210> 30
<211> 87
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (87)..(87)
<223> The 'Xaa' at location 87 stands for Ser.

<220>
<221> misc_feature
<222> (261)..(261)
<223> n = a, c, g, or t

<400> 30

Met Asp Thr Ile Pro Gln Leu Asp Ile Ser Ser Tyr Pro Ser Gln Phe
1 5 10 15

Phe Trp Phe Phe Leu Ser Phe Ser Val Leu Tyr Ile Ile Ile Ser Lys
20 25 30

Asn Val Leu Pro Lys Ile Glu Asn Ile Val Arg Lys Arg Tyr Asn Ile
35 40 45

Ile Arg Cys Ser Ile Asp Ser Val Lys Gly Asp Leu Ser His Ala Gln
50 55 60

Gln Glu Leu Asp Lys Gln Leu Leu Lys Leu Thr Ala Val Gln Ala Glu
65 70 75 80

Val Asp Arg Ile Ile Arg Xaa
85

<210> 31
<211> 3814
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 31
gatcgaggcc ccgcggaaagc tggaatcgat catgaccgcgc gcgtcggtca tggcggccgc 60
gacacgaacc tggccgacgg tgccgaccga gcgcctcgccgc gcggggggcg agatggcg 120
gggaggcgccc ggaagagcct gcatcattcc ggcactccgg gcgcgaaggc gaacagggtcc 180
gacggccgca cgaacagttc caggccccatc tggatgccga ccagcaggac gatcagcgcc 240
agaagcatac gcagtacgta cggccggAAC cggccccaca gcctcgcccc gtactgggcc 300
cccacgaccc caccgaccag caggatggtc gacaggacga tgtcgacggc ctggttgcgg 360
cccgccctgaa gaatggtggt catggcggtg acgatgatga tctggaacag gctggtgccc 420
accacgaccc cggccttcat ccgcagcaca tagagcatgg ccggcaccag aatgaagccg 480
ccgcccaccc ccatgatggc ggacaacaca ccggcgaaac cgcccagcgc gaacggggga 540

atggcgctga	tgttagaggcc	cgagcggggg	aagcgcatct	tcagcggcag	gccatacagc	600
cacatcgggc	ggcggcggttc	gccccgtggc	accacctcg	cgccacccg	cctcaggatc	660
tggccgaggc	tctcgtagag	catcagggtg	ccgatcg	cgaggaacag	cagataggac	720
accgctaccg	ccatgtccgc	ctgacccagc	agacgcagat	agcggAACAG	ttccacccccc	780
agcagcgcgc	cgaccacacc	acccaggGCC	atgacccgc	cgatgcgata	gtccaccGCC	840
ttctggctgg	tgttagctgat	cacgcccag	gtcgaggagg	cgacgacgtg	gctggcctgg	900
ctggccaccg	caaccgacgg	cgggattccg	agaaagatca	ggatcggggc	catcaggaag	960
ccccggccga	taccgaacag	tccggacacg	aatccgaccg	tcggcccag	cagaaccagg	1020
agcggccagt	tcaccgaaac	ctcgccgatc	ggcagataga	tatccaaagg	acgcgccttc	1080
ggcttggact	gaggcttaggc	gccggaaagg	cgacgacgga	agtgggtgtg	tcctagacccc	1140
accggatgg	ccccggccacc	cgatgcgc	aaaaagtca	cccgccgcgt	ccggagcgg	1200
cggcgcgacc	tggAACCGAT	cagcgtccgc	ccgggccta	ccggggccg	ccggccggcac	1260
cggagaccgc	aggcgctoga	cggccgactg	ggcgtcgata	tcccccggcgc	gcgatgcgat	1320
caggtaccat	ttttaggctt	cggtcagg	ggcgtaatg	ccgacgtctc	cggtctcata	1380
gagtttggcg	acgttgaact	ggccatcgac	cagtccgc	tcggccgagc	gtttcagcca	1440
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atcgacgaag	tccgtttcgc	cgtcgaaatc	gtcatgaccg	ccgtcaaagg	ccgacgggg	2160

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gaaccggcgca agacgcttgtt gcccctcgcaactccctcg gcgatgcgtt caatgcgacg	3660
accataggcc ctgcccgcgt cgtcctgccc ctccagtcgg cggacaaggc ccgagacggc	3720
ctgatcgacc ccctggatgg cgacgggttga gcgacgctcg gcggcgatcg gccggccgc	3780
gatggcatcg accgaggccc cgaggcgctg gatc	3814

<210> 32
<211> 810
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(810)
<223> Complement to SEQ ID NO:31, nucleotides 144..953
Similar to gas vesicle protein
Product = "12hworf1"

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ccggaaccgg cccgacagcc tcgccccgta ctgggcccc acgaccccac cgaccagcag	180	
gatggtcgac aggacgatgt cgacggtctg gttgcggccc gcctgaagaa tggtggtcat	240	
ggcggtgacg atgatgatct ggaacaggct ggtgcccacc acgaccccg cttcatccg	300	
cagcacatag agcatggccg gcaccagaat gaagccgccc cccacccca tcatggcgga	360	
caacacacccg gcaaaccgc ccagcgcgaa cggggaaatg gcgtgtatgt agaggcccg	420	
gcggggaaag cgcatttca gcggcaggcc atacagccac atcgggcccgc ggcgttcgcg	480	
gtgcggcacc acctcgccgc gcacccgcct caggatctgg ccgaggctct ctagagcat	540	
cagggtgccg atcgtgccga ggaacagcag ataggacacc gctaccgcca tgtccgcctg	600	
acccagcaga cgcagatagc ggaacagtcc caccccaagc agcgcgcgaa ccacaccacc	660	
cagggccatg accccgcccga tgcgatagtc caccgccttc tggctggtgt agctgatcac	720	
gccccaggc gaggaggcga cgacgtggct ggcctggctg gccaccgcaa ccgacggcgg	780	
gattccgaga aagatcagga tcggggccat	810	

<210> 33
<211> 2638
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(2638)
<223> Complement to SEQ ID NO:31, nucleotides 1177..>3814
Hypothetical polar organelle development protein

Product = "12hworf2i"

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gatataccccg gcgcgcgatg cgatcaggta ccatttttag gcttcggtca ggtcgggctgt	180
aatggcgacg tctccggct catagagttt ggcgacgtt aactggccat cgaccagtcc	240
gcccgtcgcc gagcgttca gccagaccag ggcctctgca cgggtctgctg aaccggccat	300
gccctcgaac aggtacatgc cgttagttata cattccggcgg gcgtcgcccc ggtcggccgc	360
gtgacgaacc cagacgcggg attcctcaag gtccacggcc aggccgttgc caccgtcatg	420
atacaggctg gccagatgca gctggggccgg ggtgttagccg gtctgggcgg cctgcttcag	480
ggtctcgact gcccggccgt cctcggcgtc cagctggacc atcgcctgtct ggttagagcac	540
ctctccggcgg gccagatcct cgggcgcagg ctgcgtcgga acaatggcca gggctgcgtat	600
cgggttagcg gtttcccccg ctgtcggcag gccgggaata ttcaggcccc atccgtcag	660
ctgtccggtc gcataggccc cgccggcggt cagcagcacg gcaatggccg aagcgccgag	720
cgccttgcga accgtgccac cgtccttgcc cgcctgttt tccagccgtt cctgaagacg	780
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gacgtccgca cgcgcgaagc cctggccgaa agcgaccgga gcagccggga tctgaaccgg	1080
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gcccgtcgacc ggcgtcgaaaga tggcgtcggc ggtcaggacc tcgggggtcg cgcgtcgac	1320
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catccgcatac cgctcgccca gttcgccgga agcgcggtcg tagccctgct cgatgcgggc 1620
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 ttccgaccgcg tccatccgct ggcgcagttc attgaccccc gagcgttgac gtcctcgat 2340
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 ctcggcgatg tcgtcaatgc gacgaccata ggccctgccc gctcgatcg gcccctccag 2520
 tcggcggaca aggccccgaga cggcctgatc gacccctgg atggcgacgg ttgagcgacg 2580
 ctcggcgatcg tgcggccggg ccgcgatggc atcgaccgag gccccgaggc gctggatc 2638

<210> 34
<211> 1698
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(1698)
<223> Corresponds to SEQ ID NO:31, nucleotides 1594..3291
Product = "12hworf3"

<400> 34
atg ata cag gct ggc cag atg cag ctg ggc cgg ggt gta gcc ggt ctg 48
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ggc ggc ctg ctt cag ggt ctc gac tgc ggc ggc gtc ctc ggc gtc cag 96
 Gly Gly Leu Leu Gln Gly Leu Asp Cys Gly Gly Val Leu Gly Val Gln
 20 25 30

ctg gac cat cgc ctg ctg gta gag cac ctc tcc gcg ggc cag atc ctc 144
 Leu Asp His Arg Leu Leu Val Glu His Leu Ser Ala Gly Gln Ile Leu
 35 40 45

ggg cgc agg ctc gct cg^g aac aat ggc cag ggc tgc gat cgg ttg agc 192
 Gly Arg Arg Leu Ala Arg Asn Asn Gly Gln Gly Cys Asp Arg Leu Ser
 50 55 60

ggt ttc ccc cgc tgt cg^g cag gcc ggg aat att cag gcc cga tcc cgt 240
 Gly Phe Pro Arg Cys Arg Gln Ala Gly Asn Ile Gln Ala Arg Ser Arg
 65 70 75 80

cag ctg tcc ggt cgc ata ggc ccc gcc ggc ggt cag cag cac ggc aat 288
 Gln Leu Ser Gly Arg Ile Gly Pro Ala Gly Gln Gln His Gly Asn
 85 90 95

ggc cga agc gcc gag cgc ctt gcg aac cgt gcc acc gtc ctt gcc cgc 336
 Gly Arg Ser Ala Glu Arg Leu Ala Asn Arg Ala Thr Val Leu Ala Arg
 100 105 110

ctg ctt ttc cag ccg ttc ctg aag acg gga ctt gcc gcc gcg ctt cag 384
 Leu Leu Phe Gln Pro Phe Leu Lys Thr Gly Leu Ala Ala Ala Leu Gln
 115 120 125

gcc gaa gcc cga acg ggc cgg agc ctc gac ggc ggg agc cgc cat ggc 432
 Ala Glu Ala Arg Thr Gly Arg Ser Leu Asp Gly Ser Arg His Gly
 130 135 140

cgc acg ggc gtc gat ggt ctg gcg ggt cga gga ggc gcg acc ctg 480
 Arg Thr Gly Gly Val Asp Gly Leu Ala Gly Arg Gly Ala Thr Leu
 145 150 155 160

ggc cgc cgc agc gcg cag ggc ccg cgg atc gac gaa gtc cgt ttc gcc 528
 Gly Arg Arg Ser Ala Gln Gly Pro Arg Ile Asp Glu Val Arg Phe Ala
 165 170 175

gtc gaa atc gtc atg acc gcc gtc aaa ggc cga cgg ggt cct gtt tcc 576
 Val Glu Ile Val Met Thr Ala Val Lys Gly Arg Arg Gly Pro Val Ser
 180 185 190

ggg cgc ggt cgc ctc caa ggc atc cga gac gtc cgc acc gcc gaa gcc 624
 Gly Arg Gly Arg Leu Gln Gly Ile Arg Asp Val Arg Thr Ala Glu Ala
 195 200 205

ctg gcc gaa agc gac cgg agc cgg gat ctg aac cgg cgg agc atc 672
 Leu Ala Glu Ser Asp Arg Ser Ser Arg Asp Leu Asn Arg Arg Ser Ile
 210 215 220

gac cgg ggc cgg ctg ggt ggc cgc gaa cgg tgg cgg cgt gaa ggc ggg 720
 Asp Arg Gly Arg Leu Gly Gly Arg Glu Arg Trp Arg Arg Glu Gly Gly
 225 230 235 240

gat ctg cgg cgg cggttccctcgac cag cga ggt cat ggt ggg Asp Leu Arg Arg Arg Ala Asp Phe Leu Gly Gln Arg Gly His Gly Gly	245	250	255	768	
tcg gct gcc gaa cgg cat cgg agc ggc gac ggg tac ctc tgc ggt cgg Ser Ala Ala Glu Arg His Arg Ser Gly Asp Gly Tyr Leu Cys Gly Arg	260	265	270	816	
tgc gag gtc ctc atc cac gcgggggccgcatgac cgc gtc gaa gat Cys Glu Val Leu Ile His Ala Gly Ala Ala His Asp Arg Val Glu Asp	275	280	285	864	
ggc gtc ggc ggt cag gac ctc ggg ggt cgc gcg ctc gac agg gaa ggg Gly Val Gly Gln Asp Leu Gly Arg Ala Leu Asp Arg Glu Gly	290	295	300	912	
cgc ggg gtc cgg ctc ggg cgg agc cag att cgc gga cca ggc ctg ctg Arg Gly Val Arg Leu Gly Arg Ser Gln Ile Arg Gly Pro Gly Leu Leu	305	310	315	320	960
ctc ggc ata gat cgg gtc gtc gaa gac tgc gtc cga gaa agg cgc atc Leu Gly Ile Asp Arg Val Val Glu Asp Cys Val Arg Glu Arg Arg Ile	325	330	335	1008	
ggg gaa ggc tgt gtc cgg aaa ggc cgc ggc ccg cca atc ggg ttc cgg Gly Glu Gly Cys Val Arg Lys Gly Arg Gly Pro Pro Ile Gly Phe Arg	340	345	350	1056	
cac ggc ggc gac cgc agt cgg aac ttc ggc ccg gcg ttc gat att gcc His Gly Gly Asp Arg Ser Arg Asn Phe Gly Pro Ala Phe Asp Ile Ala	355	360	365	1104	
acg cgc ctc ggc gat cag ggc cgc cgt gcg ctc ttc cga cat ccg cat Thr Arg Leu Gly Asp Gln Gly Arg Arg Ala Leu Phe Arg His Pro His	370	375	380	1152	
ccg ctc ggc cag ttc gcc gga agc gcg gtc gta gcc ctg ctc gat gcg Pro Leu Gly Gln Phe Ala Gly Ser Ala Val Val Ala Leu Leu Asp Ala	385	390	395	400	1200
ggc gga act gtc ggc gag acg gcg gcc gat atc gtc cag cgc ctg ctg Gly Gly Thr Val Gly Glu Thr Ala Ala Asp Ile Val Gln Arg Leu Leu	405	410	415	1248	
cga ccg ccg ctc cga ctg ggc gat gcg ttc gct cag ccg gtc gga gat Arg Pro Pro Leu Arg Leu Gly Asp Ala Phe Ala Gln Pro Val Gly Asp	420	425	430	1296	
acg ggt gat ctc ccc gcc cag ttt ttc cag ggc cag ggc atg ccg gtc Thr Gly Asp Leu Pro Ala Gln Phe Phe Gln Gly Gln Gly Met Pro Val	435	440	445	1344	
gtc ggt cgc gat cag tcg ctg ttc gat gcc ctg ggc gaa gcg gcc cat Val Gly Arg Asp Gln Ser Leu Phe Asp Ala Leu Gly Glu Ala Ala His				1392	

450

455

460

gtc ggt ctc gac ctt gcg gct cag ctg ttc gaa acg ggc cg^a aac ctc
 Val Gly Leu Asp Leu Ala Ala Gln Leu Phe Glu Thr Gly Arg Asn Leu
 465 470 475 480

gg^t ctc gat cga ctg gac ccg acc att cag gtt ctg ggc gat gcg cag
 Gly Leu Asp Arg Leu Asp Pro Thr Ile Gln Val Leu Gly Asp Ala Gln
 485 490 495

aac ctc gcg ccc cat cgc ctc gac cgc ctt ggc gga gcg ttc ctc cga
 Asn Leu Ala Pro His Arg Leu Asp Arg Leu Gly Gly Ala Phe Leu Arg
 500 505 510

cgc ctt gac ctg ctc gcc gat ggc cag gac cgc gcg ctc gat ccg gtc
 Arg Leu Asp Leu Leu Ala Asp Gly Gln Asp Arg Ala Leu Asp Pro Val
 515 520 525

cat ccg gcc ttc ggt ttc ggc tgt atc gag ccg ccg cat cat ctc ggc
 His Pro Ala Phe Gly Phe Gly Cys Ile Glu Pro Pro His His Leu Gly
 530 535 540

g^cg att ggc ttc aac cga ccg gct cag ggt ctc ggc gag ctt ttc gaa
 Ala Ile Gly Phe Asn Arg Pro Ala Gln Gly Leu Gly Glu Leu Phe Glu
 545 550 555 560

g^cg ggc ggc ctc gcg tga
 Ala Gly Gly Leu Ala
 565

<210> 35
<211> 565
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 35

Met Ile Gln Ala Gly Gln Met Gln Leu Gly Arg Gly Val Ala Gly Leu
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Gly Gly Leu Leu Gln Gly Leu Asp Cys Gly Gly Val Leu Gly Val Gln
 20 25 30

Leu Asp His Arg Leu Leu Val Glu His Leu Ser Ala Gly Gln Ile Leu
 35 40 45

Gly Arg Arg Leu Ala Arg Asn Asn Gly Gln Gly Cys Asp Arg Leu Ser
 50 55 60

Gly Phe Pro Arg Cys Arg Gln Ala Gly Asn Ile Gln Ala Arg Ser Arg

65

70

75

80

Gln Leu Ser Gly Arg Ile Gly Pro Ala Gly Gly Gln Gln His Gly Asn
85 90 95

Gly Arg Ser Ala Glu Arg Leu Ala Asn Arg Ala Thr Val Leu Ala Arg
100 105 110

Leu Leu Phe Gln Pro Phe Leu Lys Thr Gly Leu Ala Ala Leu Gln
115 120 125

Ala Glu Ala Arg Thr Gly Arg Ser Leu Asp Gly Gly Ser Arg His Gly
130 135 140

Arg Thr Gly Gly Val Asp Gly Leu Ala Gly Arg Gly Gly Ala Thr Leu
145 150 155 160

Gly Arg Arg Ser Ala Gln Gly Pro Arg. Ile Asp Glu Val Arg Phe Ala
165 170 175

Val Glu Ile Val Met Thr Ala Val Lys Gly Arg Arg Gly Pro Val Ser
180 185 190

Gly Arg Gly Arg Leu Gln Gly Ile Arg Asp Val Arg Thr Ala Glu Ala
195 200 205

Leu Ala Glu Ser Asp Arg Ser Ser Arg Asp Leu Asn Arg Arg Ser Ile
210 215 220

Asp Arg Gly Arg Leu Gly Gly Arg Glu Arg Trp Arg Arg Glu Gly Gly
225 230 235 240

Asp Leu Arg Arg Arg Ala Asp Phe Leu Gly Gln Arg Gly His Gly Gly
245 250 255

Ser Ala Ala Glu Arg His Arg Ser Gly Asp Gly Tyr Leu Cys Gly Arg
260 265 270

Cys Glu Val Leu Ile His Ala Gly Ala Ala His Asp Arg Val Glu Asp
275 280 285

Gly Val Gly Gly Gln Asp Leu Gly Gly Arg Ala Leu Asp Arg Glu Gly
290 295 300

Arg Gly Val Arg Leu Gly Arg Ser Gln Ile Arg Gly Pro Gly Leu Leu
305 310 315 320

Leu Gly Ile Asp Arg Val Val Glu Asp Cys Val Arg Glu Arg Arg Ile
325 330 335

Gly Glu Gly Cys Val Arg Lys Gly Arg Gly Pro Pro Ile Gly Phe Arg
340 345 350

His Gly Gly Asp Arg Ser Arg Asn Phe Gly Pro Ala Phe Asp Ile Ala
355 360 365

Thr Arg Leu Gly Asp Gln Gly Arg Arg Ala Leu Phe Arg His Pro His
370 375 380

Pro Leu Gly Gln Phe Ala Gly Ser Ala Val Val Ala Leu Leu Asp Ala
385 390 395 400

Gly Gly Thr Val Gly Glu Thr Ala Ala Asp Ile Val Gln Arg Leu Leu
405 410 415

Arg Pro Pro Leu Arg Leu Gly Asp Ala Phe Ala Gln Pro Val Gly Asp
420 425 430

Thr Gly Asp Leu Pro Ala Gln Phe Phe Gln Gly Gln Gly Met Pro Val
435 440 445

Val Gly Arg Asp Gln Ser Leu Phe Asp Ala Leu Gly Glu Ala Ala His
450 455 460

Val Gly Leu Asp Leu Ala Ala Gln Leu Phe Glu Thr Gly Arg Asn Leu
465 470 475 480

Gly Leu Asp Arg Leu Asp Pro Thr Ile Gln Val Leu Gly Asp Ala Gln
485 490 495

Asn Leu Ala Pro His Arg Leu Asp Arg Leu Gly Gly Ala Phe Leu Arg
500 505 510

Arg Leu Asp Leu Leu Ala Asp Gly Gln Asp Arg Ala Leu Asp Pro Val
 515 520 525

His Pro Ala Phe Gly Phe Gly Cys Ile Glu Pro Pro His His Leu Gly
 530 535 540 545

Ala Ile Gly Phe Asn Arg Pro Ala Gln Gly Leu Gly Glu Leu Phe Glu
 545 550 555 560

Ala Gly Gly Leu Ala
 565

<210> 36
 <211> 546
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(546)
 <223> Corresponds to SEQ ID NO:31, nucleotides 2789..3334
 Product = "12hworf4"

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 1 5 10 15

tgc tgc gac cgc cgc tcc gac tgg gcg atg cgt tcg ctc agc cgg tcg 96
 Cys Cys Asp Arg Arg Ser Asp Trp Ala Met Arg Ser Leu Ser Arg Ser
 20 25 30

gag ata cgg gtg atc tcc ccg ccc agt ttt tcc agg gcc agg gca tgc 144
 Glu Ile Arg Val Ile Ser Pro Pro Ser Phe Ser Arg Ala Arg Ala Cys
 35 40 45

cgg tcg tcg gtc gcg atc agt cgc tgt tcg atg ccc tgg gcg aag cgg 192
 Arg Ser Ser Val Ala Ile Ser Arg Cys Ser Met Pro Trp Ala Lys Arg
 50 55 60

ccc atg tcg gtc tcg acc ttg cgg ctc agc tgt tcg aaa cgg gcc gga 240
 Pro Met Ser Val Ser Thr Leu Arg Leu Ser Cys Ser Lys Arg Ala Gly
 65 70 75 80

acc tcg gtc tcg atc gac tgg acc cga cca ttc agg ttc tgg gcg atg 288
 Thr Ser Val Ser Ile Asp Trp Thr Arg Pro Phe Arg Phe Trp Ala Met
 85 90 95

cgc aga acc tcg cgc ccc atc gcc tcg acc gcc ttg gcg gag cgt tcc 336

Arg Arg Thr Ser Arg Pro Ile Ala Ser Thr Ala Leu Ala Glu Arg Ser			
100	105	110	
tcc gac gcc ttg acc tgc tcg ccg atg gcc agg acc gcg cgc tcg atc		384	
Ser Asp Ala Leu Thr Cys Ser Pro Met Ala Arg Thr Ala Arg Ser Ile			
115	120	125	
cgc tcc atc cgg cct tcg gtt tcg gct gta tcg agc cgc cgc atc atc		432	
Arg Ser Ile Arg Pro Ser Val Ser Ala Val Ser Ser Arg Arg Ile Ile			
130	135	140	
tcg gcg cga ttg gct tca acc gac cgg ctc agg gtc tcg gcg agc ttt		480	
Ser Ala Arg Leu Ala Ser Thr Asp Arg Leu Arg Val Ser Ala Ser Phe			
145	150	155	160
tcg aag cgg gcg gcc tcg cgt gag ccc tcg ggc tcg acc cgg gac tcg		528	
Ser Lys Arg Ala Ala Ser Arg Glu Pro Ser Gly Ser Thr Arg Asp Ser			
165	170	175	
gcg gcg cgc agc cgc tga		546	
Ala Ala Arg Ser Arg			
180			
<210> 37			
<211> 181			
<212> PRT			
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)			
<400> 37			
Met Arg Ala Glu Leu Ser Ala Arg Arg Arg Pro Ile Ser Ser Ser Ala			
1	5	10	15
Cys Cys Asp Arg Arg Ser Asp Trp Ala Met Arg Ser Leu Ser Arg Ser			
20	25	30	
Glu Ile Arg Val Ile Ser Pro Pro Ser Phe Ser Arg Ala Arg Ala Cys			
35	40	45	
Arg Ser Ser Val Ala Ile Ser Arg Cys Ser Met Pro Trp Ala Lys Arg			
50	55	60	
Pro Met Ser Val Ser Thr Leu Arg Leu Ser Cys Ser Lys Arg Ala Gly			
65	70	75	80
Thr Ser Val Ser Ile Asp Trp Thr Arg Pro Phe Arg Phe Trp Ala Met			
85	90	95	

Arg Arg Thr Ser Arg Pro Ile Ala Ser Thr Ala Leu Ala Glu Arg Ser
 100 105 110

Ser Asp Ala Leu Thr Cys Ser Pro Met Ala Arg Thr Ala Arg Ser Ile
 115 120 125

Arg Ser Ile Arg Pro Ser Val Ser Ala Val Ser Ser Arg Arg Ile Ile
 130 135 140

Ser Ala Arg Leu Ala Ser Thr Asp Arg Leu Arg Val Ser Ala Ser Phe
 145 150 155 160

Ser Lys Arg Ala Ala Ser Arg Glu Pro Ser Gly Ser Thr Arg Asp Ser
 165 170 175

Ala Ala Arg Ser Arg
 180

<210> 38
<211> 3901
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (3901)..(3901)
<223> n = a, c, g, or t

<400> 38		
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ctaaatttaa tgaattattt tattagataa tgtaagagaa aagatatagt ggttaattt		180
atatatggg aaaatatgaa agcgataaat atgataatat ttgtatacag ttatttatt		240
taattagcta atacataaga aatagctatc actatgttc aaaaaggtaa ttgtgataac		300
ttaagattgt agtttatttt atgataagtt aacttgtggc aagattggaa ttataagttt		360
tataaagaca ataaatttgta tcattatgtca acaattcctg tacctttaga tgaactggtg		420
gttattatca aatgaataat agtaagactt agtttatctc gatatgttaa tagtggtagg		480
gttgtaaaaa ttagtttaggt atggtataat atttgaaat tagtccgaaa ctattggata		540
atactgttcc tctaattaat aaagatctga aaaaggcgca ctgttataat tattgattac		600

ggtgtatttt atatagttgc ttaattctaa acattgtgta gcaacaatag tgattatgta 660
catgtaaaag actattgatt ctttgcata agctgaaagt ttatagtatt tctggatcaa 720
ggtaggtaa tcaagtgagt taaaatttc cttgaaaagc tttaaaaaaa gactagagta 780
aacatatagt tgaattatac caatgaaggg tagtcatgat aaatgtatca ttttgggtt 840
taatgtctgg aatatctgta ttatcaaaga ccacggtaat agttgttagt atttttgaag 900
gaagtaatca tttggaggat aatggtgctt tagaaggta taatgataaa atcatggaaa 960
tagtaaatgg ttatcaatct tttgatggta agtttgctga ggtattacct attattgggt 1020
tagagaaaga tttccctgtt gtggtagtta ttggactggg taaatctgag gattttgatg 1080
aaaataaaagc tttaaaagtt ggtgggtaa tatattctga acttaataga atgaaggtagc 1140
cagatgcac aattgttatt aatactgata gtaatgtaa tgccaatatt ggttatggag 1200
cactttacg tagtttaaa tttgataaat atttcgtaga gaaaaaagat aaaaattcag 1260
tttatttgaa taagttgctt ctatttcaa agagtgtatcc acaagagggtt actgctttgt 1320
ttaatgattt aaaagctgaa ggtgagtc tattcttagc tcgttctttt gtttcagagc 1380
ctccgaatat tttatatacca gaaacgtatg ctcagatgat atatgaagaa ttaagtaagg 1440
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atttatcatttcaac attaactggc gcagtagtgg ttgctttagg taataatcag tatgctggc 1980
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tcctgaaaag tttattaata agtggttata taaggttattt aatatacatc cttctctt 2820
gccatcattt aagggtttaa atgcacaagc tcaagcatta aaggctggag taaagattgc 2880
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cggtagttta gctttatcag caaaaacact acacatgttt tataatgatg aagctttgt 3120
atagcttatt ttttatgtt ttgagccttta ttttggata agttggtaaa acaatctact 3180
tttcctcgtt ataatactgt aaacaactat ttcttcgcct ttgtttgggtt ttattatgt 3240
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tttataatttt aataaaatttt gtattggttt attataacgc tataccatga atgttatttgc 3540
aagttatgtt gagtgaaaga ttgaatcctt acctgtaccc ttgataaaag ctatgtttt 3600
tatgcaacaa agggtcgagg gtattgctaa taagacacaa gatgaacttag tatggttact 3660
tgaacatttt ccgttatata cggttgtac tagtgcaagg agtgaggaat tactaaccga 3720
tagttatattt cctgtatattt ctacaggttag aggtggtaaa tacacttac atggcctgg 3780
tcaaagaatt gcttatgttga tgatggattt aaaagcaaga gataaaatgtt atgttaggtt 3840
gtatgttgaactttgggtt agtggattgt taaaacttta aagcattttt caatacgatc 3900

۱۰

3901

<210> 39
<211> 1503
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(1503)
<223> Corresponds to SEQ ID NO:38, nucleotides 816..2318
Hypothetical cytosol aminopeptidase
Product = "13hworf1"

<400> 39
atg ata aat gta tca ttt ttg ggt tta atg tct gga ata tct gta tta 48
Met Ile Asn Val Ser Phe Leu Gly Leu Met Ser Gly Ile Ser Val Leu
1 5 10 15

tta aag acc acg gta ata gtt gta ggt att ttt gaa gga agt aat cat 96
Leu Lys Thr Thr Val Ile Val Val Gly Ile Phe Glu Gly Ser Asn His
20 25 30

ttg gag gat aat ggt gct tta gaa ggt tat aat gat aaa atc atg gaa 144
 Leu Glu Asp Asn Gly Ala Leu Glu Gly Tyr Asn Asp Lys Ile Met Glu
 35 40 45

```

ata gta aat ggt tat caa tct ttt gat ggt aag ttt gct gag gta tta      192
Ile Val Asn Gly Tyr Gln Ser Phe Asp Gly Lys Phe Ala Glu Val Leu
      50          55          60

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cct att att ggg tta gag aaa gat ttt cct gtt gtg gta gtt att gga      240
Pro Ile Ile Gly Leu Glu Lys Asp Phe Pro Val Val Val Val Ile Gly
65           70                  75          80

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ctg ggt aaa tct gag gat ttt gat gaa aat aaa gct tta aaa gtt ggt
 Leu Gly Lys Ser Glu Asp Phe Asp Glu Asn Lys Ala Leu Lys Val Gly
 85 90 95

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ggt gta ata tat tct gaa ctt aat aga atg aag gta cca gat gca tca      336
Gly Val Ile Tyr Ser Glu Leu Asn Arg Met Lys Val Pro Asp Ala Ser
          100          105          110

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att gtt att aat act gat agt aat gta agt gcc aat att ggt tat gga
 Ile Val Ile Asn Thr Asp Ser Asn Val Ser Ala Asn Ile Gly Tyr Gly
 115 120 125

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gca ctt tta cgt agt ttt aaa ttt gat aaa tat ttc gta gag aaa aaa 432
Ala Leu Leu Arg Ser Phe Lys Phe Asp Lys Tyr Phe Val Glu Lys Lys
    130           135           140

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gat aaa aat tca gtt tat ttg aat aag ttg ctt cta ttt tca aag agt 480

Asp Lys Asn Ser Val Tyr Leu Asn Lys Leu Leu Leu Phe Ser Lys Ser				
145	150	155	160	
gat cca caa gag gtt act gct ttg ttt aat gat tta aaa gct gaa ggt				528
Asp Pro Gln Glu Val Thr Ala Leu Phe Asn Asp Leu Lys Ala Glu Gly				
165	170	175		
gag tca ata ttc tta gct cgt tct ttt gtt tca gag cct ccg aat att				576
Glu Ser Ile Phe Leu Ala Arg Ser Phe Val Ser Glu Pro Pro Asn Ile				
180	185	190		
tta tat cca gaa acg tat gct cag atg ata tat gaa gaa tta agt aag				624
Leu Tyr Pro Glu Thr Tyr Ala Gln Met Ile Tyr Glu Glu Leu Ser Lys				
195	200	205		
gtt ggt gta aca gtt gaa gtc ttt gat gaa gat tac atg aaa gca aat				672
Val Gly Val Thr Val Glu Val Phe Asp Glu Asp Tyr Met Lys Ala Asn				
210	215	220		
caa atg atg gca ctt ctt gga gta ggt cag ggt agt gct aaa aaa tct				720
Gln Met Met Ala Leu Leu Gly Val Gly Gln Gly Ser Ala Lys Lys Ser				
225	230	235	240	
cga ctt gta gtt atg aaa tgg aat gga ggt gat gag tca gaa agt cct				768
Arg Leu Val Val Met Lys Trp Asn Gly Gly Asp Glu Ser Glu Ser Pro				
245	250	255		
att gcg ttt gtt gga aaa ggt gta act ttt gat act ggt gga ata tcc				816
Ile Ala Phe Val Gly Lys Gly Val Thr Phe Asp Thr Gly Gly Ile Ser				
260	265	270		
tta aaa cct tca aag ggt atg tgg gat atg aaa tat gat atg gca ggt				864
Leu Lys Pro Ser Lys Gly Met Trp Asp Met Lys Tyr Asp Met Ala Gly				
275	280	285		
tct gct tct gtt gga att atg cgt act ctt gct gca agg aag gca				912
Ser Ala Ser Val Val Gly Ile Met Arg Thr Leu Ala Ala Arg Lys Ala				
290	295	300		
aaa gtt aat gct gtt gga gtg gtt gga tta gtt gaa aat tca gta gat				960
Lys Val Asn Ala Val Gly Val Val Gly Leu Val Glu Asn Ser Val Asp				
305	310	315	320	
gga aat gcg caa aga cct agt gat gtt att tca atg tct gga caa				1008
Gly Asn Ala Gln Arg Pro Ser Asp Val Val Ile Ser Met Ser Gly Gln				
325	330	335		
aca att gag gtg tta aat act gat gca gag ggt agg ttg gtt tta gct				1056
Thr Ile Glu Val Leu Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala				
340	345	350		
gat gct tta tgg tat act cag gag atg ttt act cct aaa tta atg gtg				1104
Asp Ala Leu Trp Tyr Thr Gln Glu Met Phe Thr Pro Lys Leu Met Val				
355	360	365		

gat tta gca aca tta act ggt gca gta gtg gtt gct tta ggt aat aat Asp Leu Ala Thr Leu Thr Gly Ala Val Val Val Leu Gly Asn Asn 370 375 380	1152
cag tat gct ggg ctt ttt tca aat gat gat tct att gca aat cag ttg Gln Tyr Ala Gly Leu Phe Ser Asn Asp Asp Ser Ile Ala Asn Gln Leu 385 390 395 400	1200
att gta gct ggg aat gaa tct ggt gag aaa tta tgg cgg tta cct tta Ile Val Ala Gly Asn Glu Ser Gly Glu Lys Leu Trp Arg Leu Pro Leu 405 410 415	1248
gat gaa gcc tat gat aaa ctt ata gat tca tca att gct gat atg cag Asp Glu Ala Tyr Asp Lys Leu Ile Asp Ser Ser Ile Ala Asp Met Gln 420 425 430	1296
aat att tca aca aaa gga tat ggg gcg gat agt att act gca gca cag Asn Ile Ser Thr Lys Gly Tyr Ala Asp Ser Ile Thr Ala Ala Gln 435 440 445	1344
ttc tta caa aga ttt gtt aat ggt gtt cct tgg gtg cat ttg gat att Phe Leu Gln Arg Phe Val Asn Gly Val Pro Trp Val His Leu Asp Ile 450 455 460	1392
gct ggt atg gca tgg gat tat gaa ggc act gag ata tgt cct aag ggt Ala Gly Met Ala Trp Asp Tyr Glu Gly Thr Glu Ile Cys Pro Lys Gly 465 470 475 480	1440
gca act ggt ttt ggg gta agg cta tta aat aga ttt gta tca aag tac Ala Thr Gly Phe Gly Val Arg Leu Leu Asn Arg Phe Val Ser Lys Tyr 485 490 495	1488
tat gag tct cat tag Tyr Glu Ser His 500	1503

<210> 40
<211> 500
<212> PRT
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)
<400> 40

Met Ile Asn Val Ser Phe Leu Gly Leu Met Ser Gly Ile Ser Val Leu
1 5 10 15

Leu Lys Thr Thr Val Ile Val Val Gly Ile Phe Glu Gly Ser Asn His
20 25 30

Leu Glu Asp Asn Gly Ala Leu Glu Gly Tyr Asn Asp Lys Ile Met Glu
35 40 45

Ile Val Asn Gly Tyr Gln Ser Phe Asp Gly Lys Phe Ala Glu Val Leu
50 55 60

Pro Ile Ile Gly Leu Glu Lys Asp Phe Pro Val Val Val Val Ile Gly
65 70 75 80

Leu Gly Lys Ser Glu Asp Phe Asp Glu Asn Lys Ala Leu Lys Val Gly
85 90 95

Gly Val Ile Tyr Ser Glu Leu Asn Arg Met Lys Val Pro Asp Ala Ser
100 105 110

Ile Val Ile Asn Thr Asp Ser Asn Val Ser Ala Asn Ile Gly Tyr Gly
115 120 125

Ala Leu Leu Arg Ser Phe Lys Phe Asp Lys Tyr Phe Val Glu Lys Lys
130 135 140

Asp Lys Asn Ser Val Tyr Leu Asn Lys Leu Leu Leu Phe Ser Lys Ser
145 150 155 160

Asp Pro Gln Glu Val Thr Ala Leu Phe Asn Asp Leu Lys Ala Glu Gly
165 170 175

Glu Ser Ile Phe Leu Ala Arg Ser Phe Val Ser Glu Pro Pro Asn Ile
180 185 190

Leu Tyr Pro Glu Thr Tyr Ala Gln Met Ile Tyr Glu Glu Leu Ser Lys
195 200 205

Val Gly Val Thr Val Glu Val Phe Asp Glu Asp Tyr Met Lys Ala Asn
210 215 220

Gln Met Met Ala Leu Leu Gly Val Gly Gln Gly Ser Ala Lys Lys Ser
225 230 235 240

Arg Leu Val Val Met Lys Trp Asn Gly Gly Asp Glu Ser Glu Ser Pro
245 250 255

Ile Ala Phe Val Gly Lys Gly Val Thr Phe Asp Thr Gly Gly Ile Ser
260 265 270

Leu Lys Pro Ser Lys Gly Met Trp Asp Met Lys Tyr Asp Met Ala Gly
275 280 285

Ser Ala Ser Val Val Gly Ile Met Arg Thr Leu Ala Ala Arg Lys Ala
290 295 300

Lys Val Asn Ala Val Gly Val Val Gly Leu Val Glu Asn Ser Val Asp
305 310 315 320

Gly Asn Ala Gln Arg Pro Ser Asp Val Val Ile Ser Met Ser Gly Gln
325 330 335

Thr Ile Glu Val Leu Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala
340 345 350

Asp Ala Leu Trp Tyr Thr Gln Glu Met Phe Thr Pro Lys Leu Met Val
355 360 365

Asp Leu Ala Thr Leu Thr Gly Ala Val Val Val Ala Leu Gly Asn Asn
370 375 380

Gln Tyr Ala Gly Leu Phe Ser Asn Asp Asp Ser Ile Ala Asn Gln Leu
385 390 395 400

Ile Val Ala Gly Asn Glu Ser Gly Glu Lys Leu Trp Arg Leu Pro Leu
405 410 415

Asp Glu Ala Tyr Asp Lys Leu Ile Asp Ser Ser Ile Ala Asp Met Gln
420 425 430

Asn Ile Ser Thr Lys Gly Tyr Gly Ala Asp Ser Ile Thr Ala Ala Gln
435 440 445

Phe Leu Gln Arg Phe Val Asn Gly Val Pro Trp Val His Leu Asp Ile
450 455 460

Ala Gly Met Ala Trp Asp Tyr Glu Gly Thr Glu Ile Cys Pro Lys Gly
465 470 475 480

Ala Thr Gly Phe Gly Val Arg Leu Leu Asn Arg Phe Val Ser Lys Tyr

485

490

495

Tyr Glu Ser His
500

<210> 41
<211> 639
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(639)
<223> Corresponds to SEQ ID NO:38, nucleotides 2486..3124
Hypothetical phosphoribosylamine-glycine ligase
Product = "13hworf2"

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<400> 41
atg act atg aaa cca ctt agg tta ggt att tta att tca ggt agg ggt
Met Thr Met Lys Pro Leu Arg Leu Gly Ile Leu Ile Ser Gly Arg Gly
1           5                   10                  15

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tctaatatgcaggtctgattaatgcttgtcagcga	gat	ttt	cct	96
Ser Asn Met Gln Ala Leu Ile Asn Ala Cys Gln Arg Asp Asp Phe Pro				
20	25	30		

gca agt gta tcc tgt gtt ata tca aat aaa tca aat gca aac ggt cta 144
 Ala Ser Val Ser Cys Val Ile Ser Asn Lys Ser Asn Ala Asn Gly Leu
 35 40 45

ata ctt gct cag caa agt aat att aaa act ttt ata gta caa ggt cgt
 Ile Leu Ala Gln Gln Ser Asn Ile Lys Thr Phe Ile Val Gln Gly Arg
 50 55 60

cct cta gat ttt gat gct att gat aat ata ctt gaa gaa cat gag gtg
 Pro Leu Asp Phe Asp Ala Ile Asp Asn Ile Leu Glu Glu His Glu Val
 65 70 75 80

gat tta atc tgt ctt gca gga ttt atg agt att gtt cct gaa aag ttt 288
 Asp Leu Ile Cys Leu Ala Gly Phe Met Ser Ile Val Pro Glu Lys Phe
 85 90 95

att aat aag tgg tta tat aag gtt att aat ata cat cct tct ctc ttg
 Ile Asn Lys Trp Leu Tyr Lys Val Ile Asn Ile His Pro Ser Leu Leu
 100 105 110

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cca tca ttt aag ggt tta aat gca caa gct caa gca tta aag gct gga      384
Pro Ser Phe Lys Gly Leu Asn Ala Gln Ala Gln Ala Leu Lys Ala Gly
           115          120          125

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gta aag att gct gga tgt aca gtt cat tat gta tac cca gaa gtt gat 432
Val Lys Ile Ala Gly Cys Thr Val His Tyr Val Tyr Pro Glu Val Asp

130

135

140

ggt gga cct att att gtt cag gca gca gtt cca gtg ttt tca tct gat
 Gly Gly Pro Ile Ile Val Gln Ala Ala Val Pro Val Phe Ser Ser Asp
 145 150 155 160

480

agt gtt gag gat ctt gct aat aga ata ttg aag atg gaa cat att tgt
 Ser Val Glu Asp Leu Ala Asn Arg Ile Leu Lys Met Glu His Ile Cys
 165 170 175

528

tac cct aaa gct gtg gaa cta att gct tat aat cag cta caa ctt aac
 Tyr Pro Lys Ala Val Glu Leu Ile Ala Tyr Asn Gln Leu Gln Leu Asn
 180 185 190

576

ggt agt tta gct tta tca gca aaa aca cta cac atg ttt tat aat gat
 Gly Ser Leu Ala Leu Ser Ala Lys Thr Leu His Met Phe Tyr Asn Asp
 195 200 205

624

gaa gct ttt gta tag
 Glu Ala Phe Val
 210

639

<210> 42
<211> 212
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 42

Met Thr Met Lys Pro Leu Arg Leu Gly Ile Leu Ile Ser Gly Arg Gly
 1 5 10 15

Ser Asn Met Gln Ala Leu Ile Asn Ala Cys Gln Arg Asp Asp Phe Pro
 20 25 30

Ala Ser Val Ser Cys Val Ile Ser Asn Lys Ser Asn Ala Asn Gly Leu
 35 40 45

Ile Leu Ala Gln Gln Ser Asn Ile Lys Thr Phe Ile Val Gln Gly Arg
 50 55 60

Pro Leu Asp Phe Asp Ala Ile Asp Asn Ile Leu Glu Glu His Glu Val
 65 70 75 80

Asp Leu Ile Cys Leu Ala Gly Phe Met Ser Ile Val Pro Glu Lys Phe
 85 90 95

Ile Asn Lys Trp Leu Tyr Lys Val Ile Asn Ile His Pro Ser Leu Leu

100

105

110

Pro Ser Phe Lys Gly Leu Asn Ala Gln Ala Gln Ala Leu Lys Ala Gly
115 120 125

Val Lys Ile Ala Gly Cys Thr Val His Tyr Val Tyr Pro Glu Val Asp
130 135 140

Gly Gly Pro Ile Ile Val Gln Ala Ala Val Pro Val Phe Ser Ser Asp
145 150 155 160

Ser Val Glu Asp Leu Ala Asn Arg Ile Leu Lys Met Glu His Ile Cys
165 170 175

Tyr Pro Lys Ala Val Glu Leu Ile Ala Tyr Asn Gln Leu Gln Leu Asn
180 185 190

Gly Ser Leu Ala Leu Ser Ala Lys Thr Leu His Met Phe Tyr Asn Asp
195 200 205

Glu Ala Phe Val
210

<210> 43
<211> 354
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)...(351)
<223> Corresponds to SEQ ID NO:38, nucleotides 3548..>3900
Hypothetical lipoate-protein ligase B
Product = "13hworf3i"

<220>
<221> misc_feature
<222> (354)..(354)
<223> n = a, c, g, or t

<220>
<221> misc_feature
<222> (352)..(354)
<223> Xaa = Ser

<400> 43		
atg gag tgg aag att gaa tcc tta cct gta cct tat gat aaa gct atg		48
Met Glu Trp Lys Ile Glu Ser Leu Pro Val Pro Tyr Asp Lys Ala Met		
1 5 10 15		
tgt ttt atg caa caa agg gtc gag ggt att gct aat aag aca caa gat		96
Cys Phe Met Gln Gln Arg Val Glu Gly Ile Ala Asn Lys Thr Gln Asp		
20 25 30		
gaa cta gta tgg tta ctt gaa cat ttt ccg tta tat acg gct ggt act		144
Glu Leu Val Trp Leu Leu Glu His Phe Pro Leu Tyr Thr Ala Gly Thr		
35 40 45		
agt gca agg agt gag gaa tta cta acc gat agt tta ttt cct gta tat		192
Ser Ala Arg Ser Glu Glu Leu Leu Thr Asp Ser Leu Phe Pro Val Tyr		
50 55 60		
tct aca ggt aga ggt ggt aaa tac act tat cat ggt cct ggt caa aga		240
Ser Thr Gly Arg Gly Gly Lys Tyr Thr Tyr His Gly Pro Gly Gln Arg		
65 70 75 80		
att gct tat gtg atg atg gat tta aaa gca aga gat aaa tgt aat gtt		288
Ile Ala Tyr Val Met Met Asp Leu Lys Ala Arg Asp Lys Cys Asn Val		
85 90 95		
agg ttg tat gtt gaa act ttg ggt gag tgg att gtt aaa act tta aag		336
Arg Leu Tyr Val Glu Thr Leu Gly Glu Trp Ile Val Lys Thr Leu Lys		
100 105 110		
cat ttt tca ata cga tcn		354
His Phe Ser Ile Arg		
115		
<210> 44		
<211> 117		
<212> PRT		
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)		
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<222> (354)..(354)		
<223> n = a, c, g, or t		
<220>		
<221> misc_feature		
<222> (352)..(354)		
<223> Xaa = Ser		
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Met Glu Trp Lys Ile Glu Ser Leu Pro Val Pro Tyr Asp Lys Ala Met		
1 5 10 15		

Cys Phe Met Gln Gln Arg Val Glu Gly Ile Ala Asn Lys Thr Gln Asp
 20 25 30

Glu Leu Val Trp Leu Leu Glu His Phe Pro Leu Tyr Thr Ala Gly Thr
 35 40 45

Ser Ala Arg Ser Glu Glu Leu Leu Thr Asp Ser Leu Phe Pro Val Tyr
50 55 60

Ser Thr Gly Arg Gly Gly Lys Tyr Thr Tyr His Gly Pro Gly Gln Arg
65 70 75 80

Ile Ala Tyr Val Met Met Asp Leu Lys Ala Arg Asp Lys Cys Asn Val
85 90 95

Arg Leu Tyr Val Glu Thr Leu Gly Glu Trp Ile Val Lys Thr Leu Lys
100 105 110

His Phe Ser Ile Arg
115

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<210> 45
<211> 4369
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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<212> DNA
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Hypothetical lipoprotein
Product = "14hworf2"

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<211> 3500

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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<210> 49
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Hypothetical outer membrane protein
Product = "18hworf1"

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1 5 10 15

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 Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser
 20 25 30

act aca ttg gat aag gat gca gtt ata tct ata gtt gag gaa tat ata 144
 Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
 35 40 45

acc aat tat cct cag agg gta ata gat tta ctt act aca ggc caa gca 192
 Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
 50 55 60

caa gca gaa aga gca gag ctt act gaa aat att aaa aaa tat aaa tct 240
 Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
 65 70 75 80

gag ctt gaa gat att gca tac cca tct gct ggc aat aaa gac agt aaa 288
 Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
 85 90 95

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 Ile Ala Phe Ile Glu Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
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 Met Phe Glu Asp Ile Lys Gin Ile Ile Lys Asp Gly Lys Val Arg Val
 115 120 125

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 165 170 175

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<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 50

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Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
35 40 45

Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
50 55 60

Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
65 70 75 80

Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
85 90 95

Ile Ala Phe Ile Glu Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
100 105 110

Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val
115 120 125

Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val
130 135 140

Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp
145 150 155 160

Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser
165 170 175

Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Phe Lys
180 185 190

Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser

195

200

205

Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Pro Ala Leu
210 215 220

Ile Ile Gly Asp Ala Phe Ile Gly Gly Ala Ala Asp Leu Ser Thr Leu
225 230 235 240

Arg Ser Lys Ile Val Glu Gln Gln Glu Gln
245 250

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<211> 2226
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(2226)
<223> Complement to SEQ ID NO:48, nucleotides 1275..>3500
      Product = "18hworf2i"
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<210> 52
 <211> 4750
 <212> DNA
 <213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

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agtgaccttg cattggtaac tgcttcaact ccacattgtat ctatagaagc aaaccatttt	180
ctcaaatttc caattttaac atgcacaaga ttatTTAATG taacagaaca ccctgtactc	240
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gaataccctt tctcttggc catccatatt ttccaatttat ttacaatatc atagagttct	360
ttattcgaca tacatattaa aatcaatcaa aacaaaataa tagtactatc taattaataa	420
aaaaatcctc aatagtctt agcaagaact acaaataataa tgagacactt aacttattaa	480
tatatttcaa atttattata ctactcatca tatTTAGCAT aatATCACAT ctgacatgtat	540
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gactggtttc ttgatataaa ttaggtaaaa aatgaaaatc agtatttttag gtgcaggatc	660
atTTGGCACA gcaatagcaa ttgcactgtc agcacatggt atatcagtta acttatgggg	720
acgtgatcat agaaatatta cacatataaa cacttaccga aaaaatttAA aatatttacc	780
cacatatcat ctaccagaca acatatatgc aaccagcaat atagacgaag tattatctga	840
caacaatACA tgtattatct taactattcc tacacaacaa ttacgcacca tatgtacaca	900
aatACAACAC aaacagcata tgtgtaaaaa tactccaata ttaatttGTA gtaaaggat	960
cgaaattaca tcactcaaAT ttcccagtga aatAGCAGAA gaaattttac aatataatcc	1020
aattttata ctctctggTC caagTTTGC taaAGAAATT gcagaacatc ttccTTGTAG	1080
tatAGTACTT GCTGGTgATA ataaAGAAACT tggTGAATCA ttGATAGAAA caataAGTAA	1140
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aaAGAACATA ATTGCAATTG CATGTGGAAT AATCGCTGGA aaaaatttag gtaataatgc	1260
TGTTGCTACT GTTATAACTA AAGGCATGAA TGAAATTAAA ACACATATA TAGCAAAAAA	1320
TCATTCAATA GATCTTCATA CATTAAATTGG TCCATCATGT CTTGGAGATC TAATATTAAC	1380
ATGTACAACA GAACATTCAc GCAATATGGC TTTTGGACTA GAAATAGGAA AAGGTAGAAA	1440
TATAAATACA TTAATAGATC ACAACCTAAA GCTTGTGAA GGAACCAGTA CTGTAAAACC	1500
ACTGATATCA TTGCAAAAAA ACTTAAATGT AGAACTACCA ATTGCAATAT CTATTACAA	1560
TTTATTACAT GAGAATATAT CACTAGATAA AGCCATATCA AACATATTAT CTTAGTCTAT	1620

catccttga taatttcaac acaatgataa ataaacggtc aaaaatatag aataacaacgt	1680
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atattacata acaaacttaa gtataactta aaatttccta gctaattata taaacaaatt	1800
cctatctcct atctcaatta accaattgtt atcagattat aaataagtca aattaaactt	1860
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<210> 53
 <211> 371
 <212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (1)..(371)

<223> Complement to SEQ ID NO:52, nucleotides <1..371

Hypothetical integrase/recombinase

Product = "19hworfli"

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agtgacccgg cattggtaac tgcttcact ccacattgtat atctagaagc aaaccatttt 180

ctcaaatctc caattttaac atgcacaaga ttatttaatg taacagaaca ccctgtactc 240

ttatgcaaga actctataaa cttatcaagg tctcttacat aagaaacaac tgtattcaaa 300

gaataccctt tctcttggc catccatatt ttccaattat ttacaatatc atagagttct 360

ttatttcgaca t 371

<210> 54

<211> 984

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(984)

<223> Corresponds to SEQ ID NO:52, nucleotides 632..1615

Hypothetical glycerol 3-phosphate dehydrogenase

Product = "19hworf2"

<400> 54

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Met Lys Ile Ser Ile Leu Gly Ala Gly Ser Phe Gly Thr Ala Ile Ala

1 5 10 15

att gca ctg tca gca cat ggt ata tca gtt aac tta tgg gga cgt gat 96

Ile Ala Leu Ser Ala His Gly Ile Ser Val Asn Leu Trp Gly Arg Asp

20 25 30

cat aga aat att aca cat ata aac act tac cga aaa aat tta aaa tat 144

His Arg Asn Ile Thr His Ile Asn Thr Tyr Arg Lys Asn Leu Lys Tyr

35 40 45

tta ccc aca tat cat cta cca gac aac ata tat gca acc agc aat ata 192

Leu Pro Thr Tyr His Leu Pro Asp Asn Ile Tyr Ala Thr Ser Asn Ile

50 55 60

gac gaa gta tta tct gac aac aat aca tgt att atc tta act att cct Asp Glu Val Leu Ser Asp Asn Asn Thr Cys Ile Ile Leu Thr Ile Pro 65 70 75 80	240
aca caa caa tta cgc acc ata tgt aca caa ata caa cac aaa cag cat Thr Gln Gln Leu Arg Thr Ile Cys Thr Gln Ile Gln His Lys Gln His 85 90 95	288
atg tgt aaa aat act cca ata tta att tgt agt aaa ggt atc gaa att Met Cys Lys Asn Thr Pro Ile Leu Ile Cys Ser Lys Gly Ile Glu Ile 100 105 110	336
aca tca ctc aaa ttt ccc agt gaa ata gca gaa gaa att tta caa tat Thr Ser Leu Lys Phe Pro Ser Glu Ile Ala Glu Glu Ile Leu Gln Tyr 115 120 125	384
aat cca att ttt ata ctc tct ggt cca agt ttt gct aaa gaa att gca Asn Pro Ile Phe Ile Leu Ser Gly Pro Ser Phe Ala Lys Glu Ile Ala 130 135 140	432
gaa cat ctt cct tgt agt ata gta ctt gct ggt gat aat aaa gaa ctt Glu His Leu Pro Cys Ser Ile Val Leu Ala Gly Asp Asn Lys Glu Leu 145 150 155 160	480
ggg gaa tca ttg ata gaa aca ata agt aat gat gtt cta aaa ata ata Gly Glu Ser Leu Ile Glu Thr Ile Ser Asn Asp Val Leu Lys Ile Ile 165 170 175	528
tac cat caa gat att ata ggt gta cag att gga gct gca tta aag aac Tyr His Gln Asp Ile Ile Gly Val Gln Ile Gly Ala Ala Leu Lys Asn 180 185 190	576
ata att gca att gca tgt gga ata atc gct gga aaa aat tta ggt aat Ile Ile Ala Ile Ala Cys Gly Ile Ile Ala Gly Lys Asn Leu Gly Asn 195 200 205	624
aat gct gtt gct act gtt ata act aaa ggc atg aat gaa att aaa aca Asn Ala Val Ala Thr Val Ile Thr Lys Gly Met Asn Glu Ile Lys Thr 210 215 220	672
cta tat ata gca aaa aat cat tca ata gat ctt cat aca tta att ggt Leu Tyr Ile Ala Lys Asn His Ser Ile Asp Leu His Thr Leu Ile Gly 225 230 235 240	720
cca tca tgt ctt gga gat cta ata tta aca tgt aca aca gaa cat tca Pro Ser Cys Leu Gly Asp Leu Ile Leu Thr Cys Thr Thr Glu His Ser 245 250 255	768
cgc aat atg gct ttt gga cta gaa ata gga aaa ggt aga aat ata aat Arg Asn Met Ala Phe Gly Leu Glu Ile Gly Lys Gly Arg Asn Ile Asn 260 265 270	816
aca tta ata gat cac aac cta aag ctt gtt gaa gga acc agt act gta Thr Leu Ile Asp His Asn Leu Lys Leu Val Glu Gly Thr Ser Thr Val	864

275

280

285

aaa cca ctg ata tca tta gca aaa aaa ctt aat gta gaa cta cca att
 Lys Pro Leu Ile Ser Leu Ala Lys Lys Leu Asn Val Glu Leu Pro Ile
 290 295 300

tgc ata tct att tac aat tta tta cat gag aat ata tca cta gat aaa
 Cys Ile Ser Ile Tyr Asn Leu Leu His Glu Asn Ile Ser Leu Asp Lys
 305 310 315 320

gcc ata tca aac ata tta tct tag
 Ala Ile Ser Asn Ile Leu Ser
 325

<210> 55
 <211> 327
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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Ile Ala Leu Ser Ala His Gly Ile Ser Val Asn Leu Trp Gly Arg Asp
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His Arg Asn Ile Thr His Ile Asn Thr Tyr Arg Lys Asn Leu Lys Tyr
 35 40 45

Leu Pro Thr Tyr His Leu Pro Asp Asn Ile Tyr Ala Thr Ser Asn Ile
 50 55 60

Asp Glu Val Leu Ser Asp Asn Asn Thr Cys Ile Ile Leu Thr Ile Pro
 65 70 75 80

Thr Gln Gln Leu Arg Thr Ile Cys Thr Gln Ile Gln His Lys Gln His
 85 90 95

Met Cys Lys Asn Thr Pro Ile Leu Ile Cys Ser Lys Gly Ile Glu Ile
 100 105 110

Thr Ser Leu Lys Phe Pro Ser Glu Ile Ala Glu Glu Ile Leu Gln Tyr
 115 120 125

Asn Pro Ile Phe Ile Leu Ser Gly Pro Ser Phe Ala Lys Glu Ile Ala

130

135

140

Glu His Leu Pro Cys Ser Ile Val Leu Ala Gly Asp Asn Lys Glu Leu
 145 150 155 160

Gly Glu Ser Leu Ile Glu Thr Ile Ser Asn Asp Val Leu Lys Ile Ile
 165 170 175

Tyr His Gln Asp Ile Ile Gly Val Gln Ile Gly Ala Ala Leu Lys Asn
 180 185 190

Ile Ile Ala Ile Ala Cys Gly Ile Ile Ala Gly Lys Asn Leu Gly Asn
 195 200 205

Asn Ala Val Ala Thr Val Ile Thr Lys Gly Met Asn Glu Ile Lys Thr
 210 215 220

Leu Tyr Ile Ala Lys Asn His Ser Ile Asp Leu His Thr Leu Ile Gly
 225 230 235 240

Pro Ser Cys Leu Gly Asp Leu Ile Leu Thr Cys Thr Thr Glu His Ser
 245 250 255

Arg Asn Met Ala Phe Gly Leu Glu Ile Gly Lys Gly Arg Asn Ile Asn
 260 265 270

Thr Leu Ile Asp His Asn Leu Lys Leu Val Glu Gly Thr Ser Thr Val
 275 280 285

Lys Pro Leu Ile Ser Leu Ala Lys Lys Leu Asn Val Glu Leu Pro Ile
 290 295 300

Cys Ile Ser Ile Tyr Asn Leu Leu His Glu Asn Ile Ser Leu Asp Lys
 305 310 315 320

Ala Ile Ser Asn Ile Leu Ser
 325

<210> 56

<211> 1416

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(1416)
 <223> Complement to SEQ ID NO:52, nucleotides 2467..3882
 Hypothetical nitrogen assimilation regulatory protein
 Product = "19hworf3"

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taaatactgt ctttcaaatt cttcacgagc tttacgtaat ggtacagaaa taacttagc	180
acttaaaaca tcattaatag gcgaattaga tactatatct actggtaat ctttgctgt	240
aatcatctcc ttaggagatt tcataattaa aatccattct ataacattac gtaattgtct	300
taagttacct ggccattcat atgactgcat tgctattaaa gcttcatcac ttaatacatg	360
agtacacaaa cctatTTTT tacagatgct attcataaaaa tacctacaca attccggtat	420
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caatcttcc ttggacattt caaaaatcctg tgccat 1416

<210> 57
<211> 597
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

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<220>
<221> misc_feature
<222> (1)..(597)
<223> Complement to SEQ ID NO:52, nucleotides 4154..>4750
      Hypothetical cell division protein ftsQ
      Product = "19hworf4i"
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aggtaATTtT atatttaaac cactAGACAA aataATATCC cacCAATGAC tatcaACATA 180
tgtgATAGAT gaaACCATAc cacCAACAAg agtATTATCA ttgACTACTT cacGTATAAA 240
atCTAGATGA gtTAACGCAC catCTCCATG tattGAAGTC aaATCATCCC gtATATTACA 300
attatcaaca ataATATGTC caAAACTATC aatgATAGAA tttttgttat catgataACCA 360
atTTGCAAAA gcAGAATATT ctTGAACTGT tatCTGTAAA gtATTTGGTA acAGCCTCTT 420
aACTGAGGCA tttttgatcc atggatgact agactCTATT ttGTTCTCA aatcAGCCAA 480
aggcacaAAA aAGATAGACC ttGcatcaac aAGTTACGT atttcatcAG aacttACATA 540
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<211> 4544
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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ggaaataatg gatttaaagt agaactaaat aaagtattat taaaacataa aaacatgcta 180

ccttggaaaa ttgggtatc agaattcacaa gaaagaatga cattagctat tcctccaagc 240

aaattcccaa tatttqaaaa aattatgaaa aagcatgatg ttgaaatcag tattattgga 300

acattcaata atacaaaaaa agcagtagta tcataataatg actccattat tatggatatg 360
gatataaact tcttacataa cggtatacca aaaactcatc taaaaaccat accatggtca 420
aacataatat cctcagtagt agacacatta cataataaac cactagacac tgagctaat 480
gaaatgatgc aaagaatgaa tataatgtgt aaagaattta tctctacaca atatgatcat 540
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gcaatagtta ttagaccaat actatcatca gaaaggggac tagtaaaatc acatggacta 660
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aacgaattta tatactggac ctactgtata ctatataagg aatataaaaa tacacttata	2040
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tatctatata taatgtcctc tccttactaa ttataacacc ttatgtaat actaaaatca	2160
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cctttgtaat aatttaattt aaactataga aatggcttac tcacctgaca atgatatagt	2280
agtactagca ttaggttagta attgtggcag tatgttattg aatattaaat ctgctataaa	2340
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atatgtatag tatagcaagt tatattagat tatattaaa aatacataac cagatcataa	3120
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 actaataaat ggattacgac gagTTTgtgc atcaatcatt ttctctgcta atcgacaatc 4440
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<210> 59
 <211> 1566
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(1566)
 <223> Corresponds to SEQ ID NO:58, nucleotides <1..1566
 Hypothetical phosphoribosylformylglycinamidine synthase
 Product = "21hworfli"

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1	5	10	15	
aga gat tta aac tta tat aat gca atc act gat aat gga gcc gga ggt				96
Arg Asp Leu Asn Leu Tyr Asn Ala Ile Thr Asp Asn Gly Ala Gly Gly				
20	25	30		

cta tca tct tct ata ggt gaa atg gga aat aat gga ttt aaa gta gaa Leu Ser Ser Ser Ile Gly Glu Met Gly Asn Asn Gly Phe Lys Val Glu 35 40 45	144
cta aat aaa gta tta tta aaa cat aaa aac atg cta cct tgg gaa att Leu Asn Lys Val Leu Leu Lys His Lys Asn Met Leu Pro Trp Glu Ile 50 55 60	192
tgg gta tca gaa tca caa gaa aga atg aca tta gct att cct cca agc Trp Val Ser Glu Ser Gln Glu Arg Met Thr Leu Ala Ile Pro Pro Ser 65 70 75 80	240
aaa ttc cca ata ttt gaa aaa att atg aaa aag cat gat gtt gaa atc Lys Phe Pro Ile Phe Glu Lys Ile Met Lys Lys His Asp Val Glu Ile 85 90 95	288
agt att att gga aca ttc aat aat aca aaa aaa gca gta gta tca tat Ser Ile Ile Gly Thr Phe Asn Asn Thr Lys Lys Ala Val Val Ser Tyr 100 105 110	336
aat gac tcc att att atg gat atg gat ata aac ttc tta cat aac ggt Asn Asp Ser Ile Ile Met Asp Met Asp Ile Asn Phe Leu His Asn Gly 115 120 125	384
ata cca aaa act cat cta aaa acc ata cca tgg tca aac ata ata tcc Ile Pro Lys Thr His Leu Lys Thr Ile Pro Trp Ser Asn Ile Ile Ser 130 135 140	432
tca gta gta gac aca tta cat aat aaa cca cta gac act gag cta aat Ser Val Val Asp Thr Leu His Asn Lys Pro Leu Asp Thr Glu Leu Asn 145 150 155 160	480
gaa atg atg caa aga atg aat ata tgt agt aaa gaa ttt atc tct aca Glu Met Met Gln Arg Met Asn Ile Cys Ser Lys Glu Phe Ile Ser Thr 165 170 175	528
caa tat gat cat gaa gta cag gga aca tca gtc ata aaa cct ata caa Gln Tyr Asp His Glu Val Gln Gly Thr Ser Val Ile Lys Pro Ile Gln 180 185 190	576
ggg aaa gga cga gta gat gga gaa gca ata gtt att aga cca ata cta Gly Lys Gly Arg Val Asp Gly Glu Ala Ile Val Ile Arg Pro Ile Leu 195 200 205	624
tca tca gaa agg gga cta gta aaa tca cat gga cta gga tca agc tat Ser Ser Glu Arg Gly Leu Val Lys Ser His Gly Leu Gly Ser Ser Tyr 210 215 220	672
gga gaa att agt aca tac cac atg gct gca tgt gct ata gat aca gca Gly Glu Ile Ser Thr Tyr His Met Ala Ala Cys Ala Ile Asp Thr Ala 225 230 235 240	720
ata cgt aat tat ata gca atc ggg gga aat ttc cat cac tta gca tta Ile Arg Asn Tyr Ile Ala Ile Gly Gly Asn Phe His His Leu Ala Leu 245 250 255	768

tta gat aat ttc tgt tgg tgg tgc tct aca aat cca aaa aga tta tgg Leu Asp Asn Phe Cys Trp Cys Asp Ser Thr Asn Pro Lys Arg Leu Trp 260 265 270	816
caa tta aaa aat gct gcc caa gca tgt tat gaa tac gca aaa att ttc Gln Leu Lys Asn Ala Ala Gln Ala Cys Tyr Glu Tyr Ala Lys Ile Phe 275 280 285	864
aaa aca cct ttc att tct gga aaa gat agc atg ttc aat gat ttt aaa Lys Thr Pro Phe Ile Ser Gly Lys Asp Ser Met Phe Asn Asp Phe Lys 290 295 300	912
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ctt tta att tct aca gta gga ata ata gaa aat att cac aat gcc ata Leu Leu Ile Ser Thr Val Gly Ile Ile Glu Asn Ile His Asn Ala Ile 325 330 335	1008
aca ctt gat gta aaa aat cca gga gat tta ata tac ata tta ggt gtg Thr Leu Asp Val Lys Asn Pro Gly Asp Leu Ile Tyr Ile Leu Gly Val 340 345 350	1056
aca tat gat gaa ctt gga agg tcc gaa tac caa aaa tat agc gga tta Thr Tyr Asp Glu Leu Gly Arg Ser Glu Tyr Gln Lys Tyr Ser Gly Leu 355 360 365	1104
gga aat aat aat gtt cca caa gta cgt gct aaa cat gca aaa aaa cta Gly Asn Asn Asn Val Pro Gln Val Arg Ala Lys His Ala Lys Lys Leu 370 375 380	1152
tac aag tta tat agc aat gca gtt aat aca aat att ata gca tct gca Tyr Lys Leu Tyr Ser Asn Ala Val Asn Thr Asn Ile Ile Ala Ser Ala 385 390 395 400	1200
att gca tta aac cta ggg ggg cta att ata ggt tta ata aaa tca cta Ile Ala Leu Asn Leu Gly Gly Leu Ile Ile Gly Leu Ile Lys Ser Leu 405 410 415	1248
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cat aat att gaa gat aat aac ata aaa gag aaa gta atc cta ttt tca His Asn Ile Glu Asp Asn Asn Ile Lys Glu Lys Val Ile Leu Phe Ser 435 440 445	1344
gaa tca caa agt aga att tta gta aca ata gct cca cat aat aaa caa Glu Ser Gln Ser Arg Ile Leu Val Thr Ile Ala Pro His Asn Lys Gln 450 455 460	1392
aaa ttt gaa act att ttt aaa gac ata gca cat gca aac ata ggt ata Lys Phe Glu Thr Ile Phe Lys Asp Ile Ala His Ala Asn Ile Gly Ile	1440

465	470	475	480	
atc agt gat aca aat acc ctg att att aac aat atg cac att att aat Ile Ser Asp Thr Asn Thr Leu Ile Asn Asn Met His Ile Ile Asn 485				1488
490				495
tta aat aca cta aaa cac agt tat aaa aaa ttc agc aac atg aaa ata Leu Asn Thr Leu Lys His Ser Tyr Lys Lys Phe Ser Asn Met Lys Ile 500				1536
505				510
caa gca tat gca gat gca gaa tat att tag Gln Ala Tyr Ala Asp Ala Glu Tyr Ile 515				1566
520				
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)				
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Arg Asp Leu Asn Leu Tyr Asn Ala Ile Thr Asp Asn Gly Ala Gly Gly 20 25 30				
Leu Ser Ser Ser Ile Gly Glu Met Gly Asn Asn Gly Phe Lys Val Glu 35 40 45				
Leu Asn Lys Val Leu Leu Lys His Lys Asn Met Leu Pro Trp Glu Ile 50 55 60				
Trp Val Ser Glu Ser Gln Glu Arg Met Thr Leu Ala Ile Pro Pro Ser 65 70 75 80				
Lys Phe Pro Ile Phe Glu Lys Ile Met Lys Lys His Asp Val Glu Ile 85 90 95				
Ser Ile Ile Gly Thr Phe Asn Asn Thr Lys Lys Ala Val Val Ser Tyr 100 105 110				
Asn Asp Ser Ile Ile Met Asp Met Asp Ile Asn Phe Leu His Asn Gly 115 120 125				
Ile Pro Lys Thr His Leu Lys Thr Ile Pro Trp Ser Asn Ile Ile Ser				

130

135

140

Ser Val Val Asp Thr Leu His Asn Lys Pro Leu Asp Thr Glu Leu Asn
145 150 155 160

Glu Met Met Gln Arg Met Asn Ile Cys Ser Lys Glu Phe Ile Ser Thr
165 170 175

Gln Tyr Asp His Glu Val Gln Gly Thr Ser Val Ile Lys Pro Ile Gln
180 185 190

Gly Lys Gly Arg Val Asp Gly Glu Ala Ile Val Ile Arg Pro Ile Leu
195 200 205

Ser Ser Glu Arg Gly Leu Val Lys Ser His Gly Leu Gly Ser Ser Tyr
210 215 220

Gly Glu Ile Ser Thr Tyr His Met Ala Ala Cys Ala Ile Asp Thr Ala
225 230 235 240

Ile Arg Asn Tyr Ile Ala Ile Gly Gly Asn Phe His His Leu Ala Leu
245 250 255

Leu Asp Asn Phe Cys Trp Cys Asp Ser Thr Asn Pro Lys Arg Leu Trp
260 265 270

Gln Leu Lys Asn Ala Ala Gln Ala Cys Tyr Glu Tyr Ala Lys Ile Phe
275 280 285

Lys Thr Pro Phe Ile Ser Gly Lys Asp Ser Met Phe Asn Asp Phe Lys
290 295 300

Gly Tyr Asn Asn Lys Gly Glu Pro Ile Asn Ile Ser Ala Pro Pro Ser
305 310 315 320

Leu Leu Ile Ser Thr Val Gly Ile Ile Glu Asn Ile His Asn Ala Ile
325 330 335

Thr Leu Asp Val Lys Asn Pro Gly Asp Leu Ile Tyr Ile Leu Gly Val
340 345 350

Thr Tyr Asp Glu Leu Gly Arg Ser Glu Tyr Gln Lys Tyr Ser Gly Leu
355 360 365

Gly Asn Asn Asn Val Pro Gln Val Arg Ala Lys His Ala Lys Lys Leu
370 375 380

Tyr Lys Leu Tyr Ser Asn Ala Val Asn Thr Asn Ile Ile Ala Ser Ala
385 390 395 400

Ile Ala Leu Asn Leu Gly Gly Leu Ile Ile Gly Leu Ile Lys Ser Leu
405 410 415

Ile Gly Gly Glu Leu Gly Ala Lys Ile Asp Leu Ser Leu Val Pro Thr
420 425 430

His Asn Ile Glu Asp Asn Asn Ile Lys Glu Lys Val Ile Leu Phe Ser
435 440 445

Glu Ser Gln Ser Arg Ile Leu Val Thr Ile Ala Pro His Asn Lys Gln
450 455 460

Lys Phe Glu Thr Ile Phe Lys Asp Ile Ala His Ala Asn Ile Gly Ile
465 470 475 480

Ile Ser Asp Thr Asn Thr Leu Ile Ile Asn Asn Met His Ile Ile Asn
485 490 495

Leu Asn Thr Leu Lys His Ser Tyr Lys Lys Phe Ser Asn Met Lys Ile
500 505 510

Gln Ala Tyr Ala Asp Ala Glu Tyr Ile
515 520

<210> 61

<211> 525

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(525)

<223> Corresponds to SEQ ID NO:58, nucleotides 2252..2776

Hypothetical folic acid synthesis protein

Product = "21hworf2"

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1 5 10 15				
aat tgt ggc agt atg tta ttg aat att aaa tct gct ata aat atg tta				96
Asn Cys Gly Ser Met Leu Leu Asn Ile Lys Ser Ala Ile Asn Met Leu				
20 25 30				
tct tta tat aac aaa aca tat tct tat atc tat aaa agt atg gca cta				144
Ser Leu Tyr Asn Lys Thr Tyr Ser Tyr Ile Tyr Lys Ser Met Ala Leu				
35 40 45				
tta cca gaa aat tct agt agt gat tgg gat act cct ttt ctg aat atg				192
Leu Pro Glu Asn Ser Ser Asp Trp Asp Thr Pro Phe Leu Asn Met				
50 55 60				
gta gta tca ggt tat aca aat ctt tca cca aat ctt atg tta gaa aga				240
Val Val Ser Gly Tyr Thr Asn Leu Ser Pro Asn Leu Met Leu Glu Arg				
65 70 75 80				
gtt aaa tac att gaa aaa aaa ata ggc agg ttt aat aat gaa tac tgg				288
Val Lys Tyr Ile Glu Lys Ile Gly Arg Phe Asn Asn Glu Tyr Trp				
85 90 95				
tca cct aga tgt ata gat att gac att atc tta tgg gga gat aaa gtc				336
Ser Pro Arg Cys Ile Asp Ile Asp Ile Ile Leu Trp Gly Asp Lys Val				
100 105 110				
tta gac tca caa act tta tct att cct cat aag cat atg caa gat aga				384
Leu Asp Ser Gln Thr Leu Ser Ile Pro His Lys His Met Gln Asp Arg				
115 120 125				
gat ttt gta ctt gta cca ctc tgt gat att cac gca aga ttt cct cat				432
Asp Phe Val Leu Val Pro Leu Cys Asp Ile His Ala Arg Phe Pro His				
130 135 140				
cca gta tca aag cta tca att gaa gaa ata gtt ctc aat cta cat gag				480
Pro Val Ser Lys Leu Ser Ile Glu Glu Ile Val Leu Asn Leu His Glu				
145 150 155 160				
atc aat tta ata aag cag tca tat att ata act caa tat tta tag				525
Ile Asn Leu Ile Lys Gln Ser Tyr Ile Ile Thr Gln Tyr Leu				
165 170				

<210> 62

<211> 174

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 62

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Asn Cys Gly Ser Met Leu Leu Asn Ile Lys Ser Ala Ile Asn Met Leu
 20 25 30

Ser Leu Tyr Asn Lys Thr Tyr Ser Tyr Ile Tyr Lys Ser Met Ala Leu
 35 40 45

Leu Pro Glu Asn Ser Ser Asp Trp Asp Thr Pro Phe Leu Asn Met
 50 55 60

Val Val Ser Gly Tyr Thr Asn Leu Ser Pro Asn Leu Met Leu Glu Arg
 65 70 75 80

Val Lys Tyr Ile Glu Lys Lys Ile Gly Arg Phe Asn Asn Glu Tyr Trp
 85 90 95

Ser Pro Arg Cys Ile Asp Ile Asp Ile Ile Leu Trp Gly Asp Lys Val
 100 105 110

Leu Asp Ser Gln Thr Leu Ser Ile Pro His Lys His Met Gln Asp Arg
 115 120 125

Asp Phe Val Leu Val Pro Leu Cys Asp Ile His Ala Arg Phe Pro His
 130 135 140

Pro Val Ser Lys Leu Ser Ile Glu Glu Ile Val Leu Asn Leu His Glu
 145 150 155 160

Ile Asn Leu Ile Lys Gln Ser Tyr Ile Ile Thr Gln Tyr Leu
 165 170

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<210> 63
<211> 560
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(560)
<223> Complement to SEQ ID NO:58, nucleotides 3985..>4544
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acttacaggt ttcacaggaa ctacagattt tataccagct caaaagatt ttgaagtact 180
actactttgt acttcatgct taaaagatcc tgaagaaaaa ctcatatcg ttttaactcg 240
ttgctcagta tcacacacat taaattgcat atcacatca gtatcacaaa agtaccatt 300
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atcatcatta cctttactga tagtattgtt tattatacta ataaatggat tacgacgagt 420
tttgtgcata atcattttct ctgcta atcg acaatctgtt aacttaacct gacattgcct 480
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tggagcttca tagtttgatc 560

<210> 64
<211> 4483
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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ctagaatttc actaagaata tctgcaccag ttatTCact tataccagaa ctatgagcat 180
gtataatagc tctatgaact aaccttcaa aaataatagt aggcttaact tctgagatac 240
ctttatcaat tagagtaggt atttcatac ttaaaaaatt tataatagta atttttagct 300
tatcaataga tacacgaaat gcataaaaaa cacgtctagc atctatatca tccgttaacg 360
ccaataaaaag atgttctaaa gtagcatatt catgatgaaa atcaaacgca attgataatg 420
ccttatgcaa actatcttca agatttttg ataacactaa tgtcccta atctatTTTc 480
agacactcta tcactgaaaa attaaaaata agttgcaa at gataatacat caatttcata 540
atcaatactg tgcaataat tttaatattt gtacttataa aaaacatatg ttacacaatg 600
atgcttaaac taactactta tatagtttg aaaacgatatttcaagttt ttcacactac 660
tactattaga aatcatttta ggtatagata atgtgattt tatacactt gccgttataa 720
aagtaccaga taccttacgc aacaaagtaa gatataagg actagcatta gcattaataa 780

tgcgactcg tgcattacag acagcatcg tattattgtc actaaataaa ccagtaatat 840
tcctagcaca acttcattta tcacccaata acttatttat gatatttggg ggagtattct 900
taatatatca cagcatatgt gaaatattgg atgatatttc aaaaaaagct catgataaga 960
atcttcataa cttaaatca aacccttact tagtaatact acagataata ttaatagact 1020
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tccaaactgt atttataata tccataatac ttacaatctt attttcaaag catatcatag 1140
aagcttattac aaaatacagt aacatcaaaa ctatagctgt catgtttgtc ttaatattag 1200
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taatacagta aaattaataa gcataatagg taatttattt aattcattat acaatgatat 1380
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caaagaatac tacaactata gtggtaagtt cagtttacat tgctaaagat tgttatttt 1800
acaattaaat gcctttaatt atatatatta ccgtatatgg ttatttattt tttacagtt 1860
acaatttctt tacacataaa aattttaaag tttttgttta ttatttattt ataaactaat 1920
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aaagtatatt atacttaaac ttgtgatac atatccttg cctaattata aaaaatgatt 2040
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taattaactg ataactctag cgttgcgaaa ttatcataaa tattcattttaatataaca 2460

agaataaacac ataataatat taacaatgta cactagaaaat aataactaac aagatataaa 2520
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taccataagc ttgattacct gcaacaataa tatcaccaac tttcaaggta ccttttgtt 3780
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cagcatcatg tttatcaattt ttatataaccg caactatcat agcaacatttta gctgccttta 4080

catgattaaat agattcaata gtttgtggca taataccatc atcagcggcc actactagca	4140
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gtgttatcaat aaaagttatc ttcttatctc cattcaatgt gatctggtagt gcacctatat	4260
gttgtgttat ccctttaaat tccccatcaa caacgtttga ttcacgtata gcatcaagca	4320
atgaagttt tccatgatca acatgtccca taacagtaac aactggtgct ctaggaatca	4380
attccatatt attaccatca gaatataat cattttctaa ttttagcattt tctaccaact	4440
taaatgtatg attgaacgct tctactataa tagaagcttg atc	4483

<210> 65
<211> 708
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)..(708)
<223> Corresponds to SEQ ID NO:64, nucleotides 624..1331
Hypothetical transmembrane protein
Product = "23hworf1"

<400> 65	
atg ttt gaa aac gat ata ttc aag ttt ttc aca cta cta cta tta gaa	48
Met Phe Glu Asn Asp Ile Phe Lys Phe Phe Thr Leu Leu Leu Glu	
1 5 10 15	
atc att tta ggt ata gat aat gtg att ttt ata tca ctt gcc gtt ata	96
Ile Ile Leu Gly Ile Asp Asn Val Ile Phe Ile Ser Leu Ala Val Ile	
20 25 30	
aaa gta cca gat acc tta cgc aac aaa gta aga tat ata gga cta gca	144
Lys Val Pro Asp Thr Leu Arg Asn Lys Val Arg Tyr Ile Gly Leu Ala	
35 40 45	
tta gca tta ata atg cga ctc gtt gca tta cag aca gca tcg ata tta	192
Leu Ala Leu Ile Met Arg Leu Val Ala Leu Gln Thr Ala Ser Ile Leu	
50 55 60	
ttg tca cta aat aaa cca gta ata ttc cta gca caa ctt cat tta tca	240
Leu Ser Leu Asn Lys Pro Val Ile Phe Leu Ala Gln Leu His Leu Ser	
65 70 75 80	
ccc aat aac tta ttt atg ata ttt gga gga gta ttc tta ata tat cac	288
Pro Asn Asn Leu Phe Met Ile Phe Gly Gly Val Phe Leu Ile Tyr His	
85 90 95	
agc ata tgt gaa ata ttg gat gat att tca aaa aaa gct cat gat aag	336
Ser Ile Cys Glu Ile Leu Asp Asp Ile Ser Lys Lys Ala His Asp Lys	

100

105

110

aat ctt cat aac tta aaa tca aac cct tac tta gta ata cta cag ata Asn Leu His Asn Leu Lys Ser Asn Pro Tyr Leu Val Ile Leu Gln Ile 115	120	125	384
ata tta ata gac tta gta ttc tca ata gat tca ata ctc act gct ata Ile Leu Ile Asp Leu Val Phe Ser Ile Asp Ser Ile Leu Thr Ala Ile 130	135	140	432
gga att aca tat aac att ttt ata atc caa cta gta ttt ata ata tcc Gly Ile Thr Tyr Asn Ile Phe Ile Ile Gln Leu Val Phe Ile Ile Ser 145	150	155	480
ata ata ctt aca atc tta ttt tca aag cat atc ata gaa gct att aca Ile Ile Leu Thr Ile Leu Phe Ser Lys His Ile Ile Glu Ala Ile Thr 165	170	175	528
aaa tac agt aac atc aaa act ata gct gtc atg ttt gtc tta ata tta Lys Tyr Ser Asn Ile Lys Thr Ile Ala Val Met Phe Val Leu Ile Leu 180	185	190	576
ggt atc ata cta gta cta gat gga ata cat att aaa ata tcc cat aat Gly Ile Ile Leu Val Leu Asp Gly Ile His Ile Lys Ile Ser His Asn 195	200	205	624
tat tta tat ttt acc ttt atc ttt tct agc ctc gtt gaa ata ata aat Tyr Leu Tyr Phe Thr Phe Ile Phe Ser Ser Leu Val Glu Ile Ile Asn 210	215	220	672
att ata aaa aag tca agc aat agc cta ata cag taa Ile Ile Lys Lys Ser Ser Asn Ser Leu Ile Gln 225	230	235	708
<210> 66			
<211> 235			
<212> PRT			
<213> <i>Ehrlichia ruminantium</i> (formerly <i>Cowdria ruminantium</i>)			
<400> 66			
Met Phe Glu Asn Asp Ile Phe Lys Phe Phe Thr Leu Leu Leu Glu 1	5	10	15
Ile Ile Leu Gly Ile Asp Asn Val Ile Phe Ile Ser Leu Ala Val Ile 20	25	30	
Lys Val Pro Asp Thr Leu Arg Asn Lys Val Arg Tyr Ile Gly Leu Ala 35	40	45	
Leu Ala Leu Ile Met Arg Leu Val Ala Leu Gln Thr Ala Ser Ile Leu			

50

55

60

Leu Ser Leu Asn Lys Pro Val Ile Phe Leu Ala Gln Leu His Leu Ser
 65 70 75 80

Pro Asn Asn Leu Phe Met Ile Phe Gly Gly Val Phe Leu Ile Tyr His
 85 90 95

Ser Ile Cys Glu Ile Leu Asp Asp Ile Ser Lys Lys Ala His Asp Lys
 100 105 110

Asn Leu His Asn Leu Lys Ser Asn Pro Tyr Leu Val Ile Leu Gln Ile
 115 120 125

Ile Leu Ile Asp Leu Val Phe Ser Ile Asp Ser Ile Leu Thr Ala Ile
 130 135 140

Gly Ile Thr Tyr Asn Ile Phe Ile Ile Gln Leu Val Phe Ile Ile Ser
 145 150 155 160

Ile Ile Leu Thr Ile Leu Phe Ser Lys His Ile Ile Glu Ala Ile Thr
 165 170 175

Lys Tyr Ser Asn Ile Lys Thr Ile Ala Val Met Phe Val Leu Ile Leu
 180 185 190

Gly Ile Ile Leu Val Leu Asp Gly Ile His Ile Lys Ile Ser His Asn
 195 200 205

Tyr Leu Tyr Phe Thr Phe Ile Phe Ser Ser Leu Val Glu Ile Ile Asn
 210 215 220

Ile Ile Lys Lys Ser Ser Asn Ser Leu Ile Gln
 225 230 235

<210> 67

<211> 348

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (1)..(348)

<223> Complement to SEQ ID NO:64, nucleotides 2526..2873
 Hypothetical ribosome-binding factor A
 Product = "23hworf2"

<400> 67
 ttatttagat tctaataatt ggtttactct tactaaatatta tcaaaaatgat aatcaatttt 60
 aaaatataat ttcggtacat atctaagatc tacatatgaa aatatacgct ttcttattaa 120
 aaatgaaaca tcgtttagtt cttttacaag attttcttta tctggatgat catcgaaat 180
 tacaacaaat acagtagcat ttttacatc tttactcact tctactttag atacattaac 240
 tatactacaa cctattgaat aaatatcatg tatcaatact ctcgatattg ctctgcttaa 300
 tactgaagca acctttaaat ttctaaaact ctcagattta taaatcat 348

<210> 68
 <211> 1614
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(1614)
 <223> Complement to SEQ ID NO:64, nucleotides 2870..>4483
 Hypothetical translation initiation factor IF-2
 Product = "23hworf3i"

<400> 68
 tcattgtata actctaattt cttctactat ctcaaataata ttcataacat cactttctgg 60
 atatatctct tttgaataat caagtaaaat accacattca aagccagcag taacttcctt 120
 tacatcatct ttaaatcgac gtaagacttt aatcttaccc tcatgcataa tattattatt 180
 acgaactaac ttaactaatg caccttttt taccaaacca cttgttacat aacacccaag 240
 tacactaccg ttattaccta cagaaaacac ttttctcaca gacaaagtac ctatctgtac 300
 ctcttgttcc aatggcctca acataccagt tagtatcttc ttaatatcat ctattatatc 360
 gtatataaca aaataatgct ttatttcgat atttttctgt tttgccaatt cttttacttg 420
 cgtatccggtt ttaacattaa atgctaaaat tattgaattt gatgtttccg ctaataaaac 480
 atctgacttt gtaatattcc ctacacccctt atatagaata ttaactcgta tatctttatg 540
 agtaatttta ccaattgaat aacatatagc ttctatagaa cccataacat cacactttaa 600
 gataacgttc aactcatcaa ccatacata aagcaatata ttactcttac cgattgctgg 660

ctgttactc aattccacat ttagtaaatc ttgcctataa ttaattaatt cacgtgcttg	720
tttttcagaa tctacaacaa taaaactagt accaaaattt gggacattat ttaaaccaaa	780
tacctaatt ggcattgaag gaatagcaac ttttcactc ccaccatctg cattaaacat	840
actaogcacc ctaccataag ctgattacc tgcaacaata atatcaccaa cttaaagg	900
accttttgt actattaacg tagcaactac tccacaattc ttatcaactt ttgattcaat	960
tactgtacca gatgccctag tattatatac agcttttaac tctaacaat ctgcaatcaa	1020
caatatactt gatttaact gatctaagtt tattttctcc tttgctgata caggaacaac	1080
aataacatca ctcctaaac ttctgctac cactccatgc tctaataaag cattagtaat	1140
tctatctaaa tcagcatcat gtttatcaat tttattaacc gcaactatca tagcaacatt	1200
agctgcctt acatgattaa tagattcaat agttgtggc ataataccat catcagcggc	1260
cactactagc actactatat cagtaacatt agtaccatga gctctcatag cagcaaatgc	1320
ttcatgtcct ggtgtatcaa taaaagttt ctcttatct ccattcaatg tgatctggta	1380
cgcacctata tgggtgttta tcccttaaa ttccccatca acaacgtttg attcacgtat	1440
agcatcaagc aatgaagttt ttccatgatc aacatgtccc ataacagtaa caactggtgc	1500
tcttaggaatc aattccatat tattaccatc agaatataaa tcattttcta atttagcatt	1560
gtctaccaac ttaaatgtat gattgaacgc ttctactata atagaagctt gatc	1614

<210> 69
 <211> 3829
 <212> DNA
 <213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<400> 69	
gatccagaaa attcagtgct atttcacag tctttattc cagcacatac agagttacta	60
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aaaagccgca ataaagttt tacagttct ttaggattgt acagctatcc tgtattaatg	180
gcagctgata tattacttta ccaagcaaata atagtacctg taggcattga tcaaaaacaa	240
cacttagaat tagcacgaga cattgctcaa gcttttaca caaaatacaa tacgcaatac	300
tttcaactgc cagaaccatt aattgtacag gaatcagcaa aaattatgag tttaagagac	360
ggtaaaaaaga aaatgagtaa atctgatgta tcagattatt cacgaattaa tttagaagat	420
agtaacgact taattgctca aaaaattaac aaagcaacca ctgactctat tgttagttt	480

gtacatgagt aaattcttc tgattatgct atttaataa taaaaatac tatattttgt 2220
gagaaaaata tagtaataat atgctgtaat taacacacga aaggattac ctcctgtatt 2280
tataggagat aaatccttgt acagatacca caattaaata aaacaattaa ttcatcttaa 2340
tattattat atggtttca ttagatgcc agtaaaactc tttcaccact acgaccacca 2400
aatgtaaatc ctttgctac ttctgggcta cttgttacaa ctgatccttc tgggctactt 2460
gttacaactg atccttctgg gctacttggt acaactgatc cttctggct acttggttaca 2520
actgatcctt ctgggctact tggtacaact gatccttctg ggctacttggt tacaactgat 2580
ccttctgggc tacttggtac aactgatcct tctgggctac ttgttacaac tgatccttct 2640
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gttacagttg tatcaacacc tgagatcacc ttatcatagc acacattaa tggatgaaga 3060
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ccatgaaaat ctgaaagtac gtgaccatta ctcgtaaaca taacatgata ttgcgcattga 3240
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tagaaccttg ttgtaaaaac tctgaaaaag gttccattaa atttactaca aaagaagctt 3720
gtaagctgtg atttaataca tcaagtgcac tacgttgcacc agtaacacca tgaaaatctg 3780

aaagtacgtg accattattt ataaaacataaa catgatattc cccatgatc 3829

<210> 70
<211> 780
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(780)
<223> Corresponds to SEQ ID NO:69, nucleotides <1..780
Hypothetical tryptophanyl-tRNA ligase
Product = "26hworfli"

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aca gag tta cta tgg ata ttc agt tgc att act act tca aca ggt caa cta      96
Thr Glu Leu Leu Trp Ile Phe Ser Cys Ile Thr Ser Thr Gly Gln Leu
          20           25           30

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aat aga atg actcaa ttt aaa gaa aaa agc cgc aat aaa gtt tct aca      144
Asn Arg Met Thr Gln Phe Lys Glu Lys Ser Arg Asn Lys Val Ser Thr
35          40          45

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gct tct tta gga ttg tac agc tat cct gta tta atg gca gct gat ata      192
Ala Ser Leu Gly Leu Tyr Ser Tyr Pro Val Leu Met Ala Ala Asp Ile
      50          55          60

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cac tta gaa tta gca cga gac att gct caa gct ttt aac aca aaa tac 288
 His Leu Glu Leu Ala Arg Asp Ile Ala Gln Ala Phe Asn Thr Lys Tyr
 85 90 95

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aat acg caa tac ttt caa ctg cca gaa cca tta att gta cag gaa tca      336
Asn Thr Gln Tyr Phe Gln Leu Pro Glu Pro Leu Ile Val Gln Glu Ser
          100           105           110

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gca aaa att atg agt tta aga gac ggt aaa aag aaa atg agt aaa tct 384
 Ala Lys Ile Met Ser Leu Arg Asp Gly Lys Lys Lys Met Ser Lys Ser
 115 120 125

gat gta tca gat tat tca cga att aat tta gaa gat agt aac gac tta 432
 Asp Val Ser Asp Tyr Ser Arg Ile Asn Leu Glu Asp Ser Asn Asp Leu
 130 135 140

att gct caa aaa att aac aaa gca acc act gac tct att gta ggt ttt 480
Ile Ala Gln Lys Ile Asn Lys Ala Thr Thr Asp Ser Ile Val Gly Phe

145	150	155	160	
gac ttt aca agt tta aac aat agg cct gca gta aag aat ctt gtt aat Asp Phe Thr Ser Leu Asn Asn Arg Pro Ala Val Lys Asn Leu Val Asn				528
165		170		175
att tat gct aca ctt tca aat att agt ata gaa caa aca tgt act aac Ile Tyr Ala Thr Leu Ser Asn Ile Ser Ile Glu Gln Thr Cys Thr Asn				576
180		185		190
att gca agc ttc act act aaa caa ttt aaa gaa gaa cta aca gaa tta Ile Ala Ser Phe Thr Thr Lys Gln Phe Lys Glu Glu Leu Thr Glu Leu				624
195		200		205
att att aat aac att gca cca ata cga caa aaa tta aga gag tta tta Ile Ile Asn Asn Ile Ala Pro Ile Arg Gln Lys Leu Arg Glu Leu Leu				672
210		215		220
gaa gac ata gaa tat tta cga agc ata tta atg aca gga aat aac aag Glu Asp Ile Glu Tyr Leu Arg Ser Ile Leu Met Thr Gly Asn Asn Lys				720
225		230		235
				240
gct gca tct att gca cat aag cac ata ata gaa att aaa aag att gca Ala Ala Ser Ile Ala His Lys His Ile Ile Glu Ile Lys Lys Ile Ala				768
245		250		255
gga tat tgg taa Gly Tyr Trp				780

<210> 71
<211> 259
<212> PRT
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)
<400> 71

Asp Pro Glu Asn Ser Val Leu Phe Ser Gln Ser Phe Ile Pro Ala His
1 5 10 15

Thr Glu Leu Leu Trp Ile Phe Ser Cys Ile Thr Ser Thr Gly Gln Leu
20 25 30

Asn Arg Met Thr Gln Phe Lys Glu Lys Ser Arg Asn Lys Val Ser Thr
35 40 45

Ala Ser Leu Gly Leu Tyr Ser Tyr Pro Val Leu Met Ala Ala Asp Ile
50 55 60

Leu Leu Tyr Gln Ala Asn Ile Val Pro Val Gly Ile Asp Gln Lys Gln

65

70

75

80

His Leu Glu Leu Ala Arg Asp Ile Ala Gln Ala Phe Asn Thr Lys Tyr
85 90 95

Ala Lys Ile Met Ser Leu Arg Asp Gly Lys Lys Lys Met Ser Lys Ser
115 120 125

Ile	Ala	Gln	Lys	Ile	Asn	Lys	Ala	Thr	Thr	Asp	Ser	Ile	Val	Gly	Phe
145					150					155					160

Asp Phe Thr Ser Leu Asn Asn Arg Pro Ala Val Lys Asn Leu Val Asn
165 170 175

Ile Tyr Ala Thr Leu Ser Asn Ile Ser Ile Glu Gln Thr Cys Thr Asn
 180 185 190

Ile Ala Ser Phe Thr Thr Lys Gln Phe Lys Glu Glu Leu Thr Glu Leu
195 200 205

Ile Ile Asn Asn Ile Ala Pro Ile Arg Gln Lys Leu Arg Glu Leu Leu
210 215 220

Glu Asp Ile Glu Tyr Leu Arg Ser Ile Leu Met Thr Gly Asn Asn Lys
225 230 235 240

Ala Ala Ser Ile Ala His Lys His Ile Ile Glu Ile Lys Lys Ile Ala
245 250 255

Gly Tyr Trp

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<210> 72
<211> 1056
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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<220>
 <221> misc_feature
 <222> (1)..(1056)
 <223> Complement to SEQ ID NO:69, nucleotides 2361..3416
 Similar to cell surface mucin, protein contains 9-mer tandem repe
 at
 Product = "26hworf2"

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ttctgggcta cttgttacaa ctgatccttc tgggctactt gttacaactg atccttctgg	120
gctacttggtt acaaactgatc cttctggct acttgggttaca actgatcctt ctgggctact	180
tgttacaact gatccttctg ggctacttgt tacaactgtat ctttctggc tacttggta	240
aactgatcct tctgggctac ttgttacaac tgatccttct gggctacttg ttacaactga	300
tccttctggg ctacttgttca caactgatcc ttctgggcta cttgttacaa ctgatccttc	360
tgggctactt gttacaactg atccttctgg gctacttgtt acaaactgatc cttctggct	420
acttgggttaca actgatcctt ctgggctact tggttacaact gatccttctg ggctacttgt	480
tacaactgtat ctttctggc tacttggta aactgatcct tctgggctac ttgttacaac	540
tgatccttct gggctacttg ttacaactga tccttctggg ctacttgttca caactgatcc	600
ttctgggcta cttgttacag ctgatccttc tgggctattt gttacagttg tatcaacacc	660
tgagatcacc ttatcatagc acacattaa tggatgaaga ttaagagaaa aattagaacc	720
ttgttgtaaa aactctgaaa aaggttccat taaatttact aaaaaagaag cttgtaaagct	780
gtggtttaat acatcaagtg caatatgttt accagtaaca ccatgaaaat ctgaaagtac	840
gtgaccatta ctcgtaaaca taacatgata ttgcgcattga tgatcccattt gaccttcttc	900
atgctcatga ggatgatagc caatctccat tgtaatatca ccatttggaaa cagagaattg	960
attattacta tagatactta aatcatttcc aaaatcaata ttgtcaattc ttgttggtaa	1020
atgaagcata caatcttctg ctgttgaatg aaccat	1056

<210> 73
 <211> 300
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

 <220>
 <221> misc_feature

<222> (1)..(300)
<223> Complement to SEQ ID NO:69, nucleotides 3530..>3829
Similar to 26hworf2
Product = "26hworf3i"

<400> 73
ttacgaagat acagatgtaa attcgctatt ttgagaagcc gtatcagtaa cagataactaa 60
attagcactt acacaatcaa cattatgatt gtggcaatct tctgttaatg gatgaagatt 120
aagagaaaaaa ttagaacctt gttgtaaaaaa ctctgaaaaa ggttccatta aatttactac 180
aaaagaagct tgtaagctgt gatthaatac atcaagtgc aatatgtgac cagtaacacc 240
atgaaaaatct gaaagtacgt gaccatttataaaacata acatgatatt ccccatgatc 300

<210> 74
<211> 4460
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 74
gatcaattat tagtgcttc tgttagttgat tgtatggaat attttgctaa cttagtcaat 60
aagcgtatta ctagtaaagt gaaacgttat atttctataat taagtacttc tatataatgac 120
gtgtctgttg ttgagttatt taatcggcgt aacaatataa tagatagaat gttgtgctaa 180
aaggatattt tatatttgtg taaaaggatt ttatataatg ggttcctaatt taacatttgt 240
gaattaaaac atattttaa taaattcttt atatgtgtac tacatagtga aatagtaaat 300
cttgcgttgt tataaattca tacttttca ctttcaattt aataacgtca ttttctggat 360
aaatagttat gaaactttct ttgtatataatg ttagtactat aggtgtgatt atattgttac 420
tttgcgttgat gtttaattttg tattgtatcg atattgcata tgctaattt aaaaactgtg 480
ttttcaataa tactgataaa actaaaaatg ctgtgaattt atctattgaa aacagggta 540
aaaactctgt ttatgttgtt ctaaaaaaaag aattnagaag tacattaaga aatttttgtg 600
attataacaa tggtaactct gtggaaagcaa aatctgtcata atatgtgtat ctgtatgtaa 660
aagctggttc taaatacatc caagatttaa tatctgaaat agatgaccga attgttaatc 720
agtatattac tgggagggtt ttatcactag aagtattaaat aatgcaattt gaggatcaa 780
tatataactat atgtaatgag gaaactatac agtgcgaact acaaagagtg ctatatgtac 840
gtttgcgttt aaataatatt taaaagttga caaaaagtat atgtgaacaa agtgtatattg 900
aattatggaa aatataatggaa atgaaatttg aatatgcattt atcttttatt catagtggtt 960

ttacttataat aatgaaaaat atatgtacat taagtggtaa tgtttattgt aataatcaaa 1020
aacagttgtg tactgatgat gttactttta ctactatatc attatatgt ataaaccatt 1080
gtatttagtca ttagataaaat ttctaaagctt tatttgattt tggtatgtgg aatgttcaaa 1140
tatttaggtta attttattca cttagataag tagtgtctat tggtataaaat taacttgtgc 1200
tttttattct ataaattgtat atagtgtatg tctaattgcgt taattcttaa ctatcttgg 1260
cagtgtaa ttatttatt tgctaatttt tactgatgtg aaaagtaaat attgatatgt 1320
aagttatgtat atattattta attactaatt tcagttatgt tgcatatgt tgacataact 1380
gtatattaa aattatgtat tagtataatt ttattcaaca gttttgttaa actaagatgt 1440
aatttagttt gttgtaagtg tagtatttca atttttaatt tttgatataat taatgttagc 1500
taggtatata ataaattgtat tatttgatatac aaaaaatattt agtactattt attatataca 1560
tgatcaaattt tgttataattt gtaagggAAC taaatgagag tttcattttat gttagagaata 1620
tgattgtgt tttattgttag tcaatatttc ttgacatttt tactagttat atttttattt 1680
gtttgtgata cgtaataaca agatatttga aaatataat agactactaa tttagttatc 1740
aaaaaaataaaa gttttatata ttaaatctag tattaaagaa ataaagaattt ataaacccgtat 1800
atgttaagtt atgtgataag gtaacggattt taacaagagc tggtttttt aacttttatg 1860
ttatattaat gtattattta tatgtacata ttatggatca attgggtgtat ataaattagg 1920
atgatagatc tcaagtatct ttttatattt tgtaattttt tattgtttt atcttcattgc 1980
taacatcagt actagttattt ttagagaagt agtattaaag tacaggtttt tatagtttat 2040
tttttaatttt tagctgttca tattgagttt acataatgt ttaagtatgt tatggcttat 2100
ggaatttatttta aaggtattttt aagtttttattt aagtttttattt aagtttttattt 2160
aggtactagt ttgggtgtcaa tgtattgttag tgaagtaacg tcaggaattt caaatctcca 2220
gaatttatctt gttgccttac taatgcctat tctgggggtt caaatataat catctatatt 2280
gagatttggta ttacaaatgc agaaactatg atttgctgtc atgtctatat tggtatgttc 2340
ttttgttatg tttttttttt tacatattttt tctgggttca ttaactttt tttttttttt 2400
attttttagat aataagatattttt tacttcgaat taatattgtc gcaggaaac cttcagggttc 2460
tgtaacaacg ttgaggcagt gatacattcc atagattaaa taaacataag agaatccagg 2520
gttaccaaac attacagcag tgcgtttgtt atatccgtgg aaagaatgtg ctgcattgtc 2580

atctttgcctt atatatgttt ctgttttgtt tataatccct ttgtgttgat taaaaagtaa 2640
catcttcgcctt agtaagctgc ttgcaacatc aagtgatttt tggttataaa atgacttctt 2700
taatatgtt tacatgttatt gtcttttatca ctactatggg actatttaca actaattata 2760
tttagtgatgt ataatttttg tcaattaatg gaaatgagct atggatagtg tgaagaagg 2820
gttagatattt tgtaaatata aaaaagctat gtgcattata atagaatacg aaatgtattt 2880
tacaaaatta cattttattat tggtgatatc taagtatagg tttaagaata tgcatacg 2940
ttcaatatta aagtaagata ctataggta aatttagttt cgtataaaat attaatgcta 3000
tagaaggata aattgattaa ggaatattt tagtatttaa gtaacgtgac tatccatatt 3060
tagttatatt ataatggtaa taattatgaa agtattgttt aatgttatct aaattataat 3120
gtttttaagt tttcaagttac agttagtaat ttgttgaaa catataat tccataagtt 3180
tttttagtgg cttagttat gatatgtgta ctttgcataa gaacttttagt aacattattt 3240
aattagggtta aattgattta tttagcattat aaagattttt ataaattgtt caactattcc 3300
tacattaatt acctataggg ttattgattt ttcatattat tggatgtat actcccatgt 3360
gttactgatt aatgggtgtt tatgccgtat agagattttt ctataacttg gtttagctata 3420
ttgatagcgt gtatcatcac gatatgtgta ctaatacatg tgctatgttag gtatgcgttt 3480
cctgatctca aaacacgtct agaacggaa agaaaagcac aggcaaaaat ggataagtt 3540
cttgctaaac aaaacgagtc attagttat aataaacaag aagaaaagag tgaaaaagag 3600
cctgacatat tggatgttcc tttagtccat ccattttttt ggcattgttc aaattcagat 3660
aaattgttcc tttagtccat ccattttttt ggcattgttc aaattcagat 3720
cagctaccac aacttgcgtc tagccctact gtagttgatc aagatgagat aagtcaagtt 3780
gagtctacaa tggatgttcc tttagtccat ccattttttt ggcattgttc aaattcagat 3840
acttctcttag tttagtgcgtt tatcattgttcc tttagtccat ccattttttt ggcattgttc 3900
ttttttttttt tagtaaaggaa gaatcgttcc tttagtccat ccattttttt ggcattgttc 3960
tggtgtcaaa gatagaaaat gtgttagaaa agaattactt atagaagtta tataattttt 4020
tttagtatct aatgtttttt tagtaaaggaa gaatcgttcc tttagtccat ccattttttt 4080
agtctcatga aaatgtatgtt atcaaaattgtt taatgtatcatac ataaggctta tttttttttt 4140
aatctgtata acgttttata ttcttttttag tttagtgcgtt tatcattgttcc tttagtccat 4200
tactctaaat tccatgttcc tttagtccat ccattttttt ggcattgttc aaattcagat 4260

atgattttgc tgttatataat	4320
tgtatataat gtagtgttatt agttaaataa tggctgtat tatgcattct	4380
ctttagctat tataaggttca gtaggtttag cactaatcat actttgtta tgtgttagtc	4440
aaccttatcaa atatgcgatc	4460

<210> 75
<211> 726
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(726)
<223> Corresponds to SEQ ID NO:74, nucleotides 369..1094
Hypothetical outer membrane protein
Product = "27hworf1"

<400> 75	
atg aaa ctt tct ttg tat ata gtt agt act ata ggt gtg att ata ttg	48
Met Lys Leu Ser Leu Tyr Ile Val Ser Thr Ile Gly Val Ile Ile Leu	
1 5 10 15	
tta ctt tgc ttg atg tta att ttg tat tgt atc gat att gca tat gct	96
Leu Leu Cys Leu Met Leu Ile Leu Tyr Cys Ile Asp Ile Ala Tyr Ala	
20 25 30	
aat att aaa aac tgt gtt ttc aat aat act gat aaa act aaa aat gct	144
Asn Ile Lys Asn Cys Val Phe Asn Asn Thr Asp Lys Thr Lys Asn Ala	
35 40 45	
gtg aat tta tct att gaa aac agg gtt aaa aac tct gtt tta tgt ggt	192
Val Asn Leu Ser Ile Glu Asn Arg Val Lys Asn Ser Val Leu Cys Gly	
50 55 60	
cta aaa aaa gaa ttt aga agt aca tta aga aat ttt tgt gat tat aac	240
Leu Lys Glu Phe Arg Ser Thr Leu Arg Asn Phe Cys Asp Tyr Asn	
65 70 75 80	
aat gtt aac tct gta gaa gca aaa tct gct caa tat ggt agt ctg atg	288
Asn Val Asn Ser Val Glu Ala Lys Ser Ala Gln Tyr Gly Ser Leu Met	
85 90 95	
gta aaa gct ggt tct aaa tac atc caa gat tta ata tct gaa ata gat	336
Val Lys Ala Gly Ser Lys Tyr Ile Gln Asp Leu Ile Ser Glu Ile Asp	
100 105 110	
gac cga att gtt aat cag tat att act ggg agg gta tta tca cta gaa	384
Asp Arg Ile Val Asn Gln Tyr Ile Thr Gly Arg Val Leu Ser Leu Glu	
115 120 125	

gta tta ata atg caa ttt gag gat aca ata tat act ata tgt aat gag Val Leu Ile Met Gln Phe Glu Asp Thr Ile Tyr Thr Ile Cys Asn Glu 130 135 140	432
gaa act ata cag tgc gaa cta caa aga gtg cta tat gta cgt ttg ctt Glu Thr Ile Gln Cys Glu Leu Gln Arg Val Leu Tyr Val Arg Leu Leu 145 150 155 160	480
tta aat aat att tta aag ttg aca aaa agt ata tgt gaa caa agt gat Leu Asn Asn Ile Leu Lys Leu Thr Lys Ser Ile Cys Glu Gln Ser Asp 165 170 175	528
att gaa tta atg gaa ata tat gga atg aaa ttt gaa tat gct tta tct Ile Glu Leu Met Glu Ile Tyr Gly Met Lys Phe Glu Tyr Ala Leu Ser 180 185 190	576
ttt att cat agt ggt ttt act tat ata atg aaa aat ata tgt aca tta Phe Ile His Ser Gly Phe Thr Tyr Ile Met Lys Asn Ile Cys Thr Leu 195 200 205	624
agt ggt aat gtt tat tgt aat aat caa aaa cag ttg tgt act gat gat Ser Gly Asn Val Tyr Cys Asn Asn Gln Lys Gln Leu Cys Thr Asp Asp 210 215 220	672
gtt act ttt act act ata tca tta tat gat ata aac cat tgt att agt Val Thr Phe Thr Thr Ile Ser Leu Tyr Asp Ile Asn His Cys Ile Ser 225 230 235 240	720
cat tag His	726

<210> 76
<211> 241
<212> PRT
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<400> 76

Met Lys Leu Ser Leu Tyr Ile Val Ser Thr Ile Gly Val Ile Ile Leu
1 5 10 15

Leu Leu Cys Leu Met Leu Ile Leu Tyr Cys Ile Asp Ile Ala Tyr Ala
20 25 30

Asn Ile Lys Asn Cys Val Phe Asn Asn Thr Asp Lys Thr Lys Asn Ala
35 40 45

Val Asn Leu Ser Ile Glu Asn Arg Val Lys Asn Ser Val Leu Cys Gly
50 55 60

Leu Lys Lys Glu Phe Arg Ser Thr Leu Arg Asn Phe Cys Asp Tyr Asn
65 70 75 80

Asn Val Asn Ser Val Glu Ala Lys Ser Ala Gln Tyr Gly Ser Leu Met
85 90 95

Val Lys Ala Gly Ser Lys Tyr Ile Gln Asp Leu Ile Ser Glu Ile Asp
100 105 110

Asp Arg Ile Val Asn Gln Tyr Ile Thr Gly Arg Val Leu Ser Leu Glu
115 120 125

Val Leu Ile Met Gln Phe Glu Asp Thr Ile Tyr Thr Ile Cys Asn Glu
130 135 140

Glu Thr Ile Gln Cys Glu Leu Gln Arg Val Leu Tyr Val Arg Leu Leu
145 150 155 160

Leu Asn Asn Ile Leu Lys Leu Thr Lys Ser Ile Cys Glu Gln Ser Asp
165 170 175

Ile Glu Leu Met Glu Ile Tyr Gly Met Lys Phe Glu Tyr Ala Leu Ser
180 185 190

Phe Ile His Ser Gly Phe Thr Tyr Ile Met Lys Asn Ile Cys Thr Leu
195 200 205

Ser Gly Asn Val Tyr Cys Asn Asn Gln Lys Gln Leu Cys Thr Asp Asp
210 215 220

Val Thr Phe Thr Thr Ile Ser Leu Tyr Asp Ile Asn His Cys Ile Ser
225 230 235 240

His

<210> 77

<211> 567

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(567)
<223> Complement to SEQ ID NO:74, nucleotides 2149..2715
Hypothetical DNA-3-methyladenine glycosidase
Product = "27hworf2"

<400> 77
ttaagttagt gtaggtacta gtttggtgtc aatgtattgt agtgaagtaa cgtcaggaat 60
tacaaatctc cagaatttat ctgttgcctt actaatgcct attctgggg tgcaaata 120
atcatctata ttgagattt tattacaat gcagaaacta tgatttgctg tcattgtctat 180
attgttatgt tcttttgta tgtgtagggt tttacatatt tttcctggtc cattaacttt 240
tgtatgtgggt gtatTTTtag ataataagat tatacttcga attaatattt ctgcaggaa 300
accttcaggt tctgttaacaa cggttggca gtgatacatt ccatagatta aataaacata 360
agagaatcca gggttaccaa acattacagc agtgcgcctt gtatatccgt ggaaagaatg 420
tgctgcttga tcattttgtc ctatatatgc ttctgtttct gttataatcc ctttgttttg 480
attaaaaagt aacatcttgc cttagtaagct gcttgcacaa tcaagtgatt tttgtttata 540
aaatgacttc tttaatatgt tgtacat 567

<210> 78
<211> 240
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(240)
<223> Complement to SEQ ID NO:74, nucleotides 3369..3608
Product = "27hworf4"

<400> 78
ttaatggtgt gttatgccgt atagagattt tgctataact tggtagcta tattgatagc 60
gtgtatcatc acgatatgt tactaataaca tgtgctatgt aggtatgcgt ttcctgatct 120
caaaaacacgt ctagaacggg aaagaaaaagc acaggcaaaa atggataagt tacttgctaa 180
acaaaaacgag tcattagtta ataataaaca agaagaaaaag agtggaaaag agcctgacat 240

<210> 79
<211> 519
<212> DNA

<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>

<221> CDS

<222> (1)..(519)

<223> Corresponds to SEQ ID NO:74, nucleotides 3382..3900
Hypothetical lipoprotein
Product = "27hworf3"

<400> 79

atg ccg tat aga gat ttt gct ata act tgg tta gct ata ttg ata gcg	48
Met Pro Tyr Arg Asp Phe Ala Ile Thr Trp Leu Ala Ile Leu Ile Ala	
1 5 10 15	

tgt atc atc acg ata tgt gta cta ata cat gtg cta tgt agg tat gcg	96
Cys Ile Ile Thr Ile Cys Val Leu Ile His Val Leu Cys Arg Tyr Ala	
20 25 30	

ttt cct gat ctc aaa aca cgt cta gaa cg ^g gaa aga aaa gca cag gca	144
Phe Pro Asp Leu Lys Thr Arg Leu Glu Arg Glu Arg Lys Ala Gln Ala	
35 40 45	

aaa atg gat aag tta ctt gct aaa caa aac gag tca tta gtt aat aat	192
Lys Met Asp Lys Leu Leu Ala Lys Gln Asn Glu Ser Leu Val Asn Asn	
50 55 60	

aaa caa gaa gaa aag agt gaa aaa gag cct gac ata ttg tca gaa ggt	240
Lys Gln Glu Lys Ser Glu Lys Pro Asp Ile Leu Ser Glu Gly	
65 70 75 80	

gat act cag cca tta gga tgc cat tgt tca aat tca gat aaa ttg aat	288
Asp Thr Gln Pro Leu Gly Cys His Cys Ser Asn Ser Asp Lys Leu Asn	
85 90 95	

gat gag tct gta gag ttg cta gag gaa caa cag gat caa cta cag agt	336
Asp Glu Ser Val Glu Leu Leu Glu Gln Gln Asp Gln Leu Gln Ser	
100 105 110	

gaa cag cta cca caa ctt gtg tct agc cct act gta gtt gaa caa gat	384
Glu Gln Leu Pro Gln Leu Val Ser Ser Pro Thr Val Val Glu Gln Asp	
115 120 125	

gag ata agt caa gtt gag tct aca atg gaa ggg tta cat cct act ggt	432
Glu Ile Ser Gln Val Glu Ser Thr Met Glu Gly Leu His Pro Thr Gly	
130 135 140	

tca ccg tgt tgt cga aga cgg gct cta act tct cta gtt agt gat gtt	480
Ser Pro Cys Cys Arg Arg Ala Leu Thr Ser Leu Val Ser Asp Val	
145 150 155 160	

atc att gag caa cag ggt aat agc caa ggt aag gag tag	519
Ile Ile Glu Gln Gln Gly Asn Ser Gln Gly Lys Glu	
165 170	

<210> 80
<211> 172
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 80

Met Pro Tyr Arg Asp Phe Ala Ile Thr Trp Leu Ala Ile Leu Ile Ala
1 5 10 15

Cys Ile Ile Thr Ile Cys Val Leu Ile His Val Leu Cys Arg Tyr Ala
20 25 30

Phe Pro Asp Leu Lys Thr Arg Leu Glu Arg Glu Arg Lys Ala Gln Ala
35 40 45

Lys Met Asp Lys Leu Leu Ala Lys Gln Asn Glu Ser Leu Val Asn Asn
50 55 60

Lys Gln Glu Glu Lys Ser Glu Lys Glu Pro Asp Ile Leu Ser Glu Gly
65 70 75 80

Asp Thr Gln Pro Leu Gly Cys His Cys Ser Asn Ser Asp Lys Leu Asn
85 90 95

Asp Glu Ser Val Glu Leu Leu Glu Gln Gln Asp Gln Leu Gln Ser
100 105 110

Glu Gln Leu Pro Gln Leu Val Ser Ser Pro Thr Val Val Glu Gln Asp
115 120 125

Glu Ile Ser Gln Val Glu Ser Thr Met Glu Gly Leu His Pro Thr Gly
130 135 140

Ser Pro Cys Cys Arg Arg Ala Leu Thr Ser Leu Val Ser Asp Val
145 150 155 160

Ile Ile Glu Gln Gln Gly Asn Ser Gln Gly Lys Glu
165 170

<210> 81
<211> 560
<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (560)..(560)

<223> n = a, c, g, or t

<400> 81

gatccataat ctcatcaata acccctgtaa ttgaggtatt agtagaaata ttagctatat	60
---	----

cacaccaagc attttcaata atttcttaa aatcagaagt atttaccata ttcacatacc	120
--	-----

tcaacttaac aacacagatt tattattata aacactatta aaaaataaac aagatacaca	180
---	-----

ctatgaatca gataaccttg gtattcta atacgtatga tataatgata ctaaaccata	240
---	-----

agtttatatt atttaaagac ataatgacat atctttaat gctaataatgt ataatcttaa	300
---	-----

agtccttaag atacatacat ttatagacat atctgtaata atgcactata taatgttaag	360
---	-----

atgtatagc aataagtttg tgTTTaatga gaatagaatg caaaaattgc aaaggcagttt	420
---	-----

atagaataga caatagcaaa attcccatta atggtaaaaa agttaaagtt aaatgcacaa	480
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actgtataac tacatggatg cacataccaa ctcaagataa agcaataacct gaagaagaaa	540
--	-----

aacaattagt aataggatcn	560
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<210> 82

<211> 174

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(174)

<223> Corresponds to SEQ ID NO:81, nucleotides 387..>559

Product = "1gdorf1i"

<220>

<221> misc_feature

<222> (174)..(174)

<223> n = a, c, g, or t.

<220>

<221> misc_feature

<222> (172)..(174)

<223> Xaa = Ser

<400> 82

atg aga ata gaa tgc aaa aat tgc aaa gca gtt tat aga ata gac aat Met Arg Ile Glu Cys Lys Asn Cys Lys Ala Val Tyr Arg Ile Asp Asn 1 5 10 15	48
agc aaa att ccc att aat ggt aaa aaa gtt aaa tgc aca aac Ser Lys Ile Pro Ile Asn Gly Lys Lys Val Lys Val Lys Cys Thr Asn 20 25 30	96
tgt aat act aca tgg atg cac ata cca act caa gat aaa gca ata cct Cys Asn Thr Thr Trp Met His Ile Pro Thr Gln Asp Lys Ala Ile Pro 35 40 45	144
gaa gaa gaa aaa caa tta gta ata gga tcn Glu Glu Glu Lys Gln Leu Val Ile Gly Xaa 50 55	174

<210> 83
<211> 58
<212> PRT
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> misc_feature
<222> (58)..(58)
<223> The 'Xaa' at location 58 stands for Ser.

<220>
<221> misc_feature
<222> (174)..(174)
<223> n = a, c, g, or t.

<220>
<221> misc_feature
<222> (172)..(174)
<223> Xaa = Ser

<400> 83

Met Arg Ile Glu Cys Lys Asn Cys Lys Ala Val Tyr Arg Ile Asp Asn 1 5 10 15
--

Ser Lys Ile Pro Ile Asn Gly Lys Lys Val Lys Val Lys Cys Thr Asn 20 25 30

Cys Asn Thr Thr Trp Met His Ile Pro Thr Gln Asp Lys Ala Ile Pro 35 40 45

Glu Glu Glu Lys Gln Leu Val Ile Gly Xaa 50 55
--

<210> 84
<211> 2008
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 84
gatcaaaaag ggataccaaa agagcaatac tatataaaat tagtatctgt taattcaaca 60
tatcctgact caattaataa cttactcata ttttagtagta ttattgaaag ctatgaaggc 120
actgtgaaca aatttcgttg tggagatact gtaagtataa agtacgatat acgtgaacta 180
aacggtaata cgatactaca agatcaagaa taaaattta ctattggaaa aaatgaagtc 240
cctcttgcaa tagagctagg tgtaattaat atgagacaag acatggcaag acatattatt 300
gcaccattag aacttttgac taattttgac aaacctgaca acttttgatg aataaaaaat 360
aaaactaatt gatattaccc acattaatca accacaacct ataaaaaaa acgcaaagcc 420
cagccatct taaggtgatt atttcttata tctgtatagc cacataaaaa agctaaaaat 480
aacgttatta tatcaaataa attacaatca acaatactac actaatatta tagaaatcta 540
ctaatatatt gatatacgaa aataatacac atttacacaa tcaatactta aattcataat 600
aacttgcgtc aactttataa aaccagctat ttcataaaaa taacacaaaa ctataaaaca 660
ccaaatagct tactcacgct aatgtttct ataaataat caacttgttta ttgtataat 720
ataaaaaactc accaattttta ataaaaacaaa tatatactaa tcttttattt cctaatttat 780
cttaataaga ttcaatatcc ttatactaat acaaatctt actcatatat taccacccca 840
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gtaactgagg tatttaagac atttaataat tatataccat ataaaaatct gcttaatgtt 1200
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cataatcaaaa tctgcttaat gtactagcaa ttgatggatt attctctcat aatatatgt	1560
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gtactagcaa ttgacaacta tgccctgata atctatgtat cataaaatac ctcatttaac	1740
aaaactttat ctattctata accttaacta ttaccatttt taagtaactg aagtattttaa	1800
gatatttgac aattatataat catataaaaaa tctttaatgt actagaatt gacaactatt	1860
ccctgataat ctatgttagca taaaataacct acaggaatct ttattaatag taatttactt	1920
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<210> 85
<211> 348
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

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<220>
<221> CDS
<222> (1)..(348)
<223> Corresponds to SEQ ID NO:84, nucleotides <1..348
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gtt aat tca aca tat cct gac tca att aat aac tta ctc ata ttt agt
 Val Asn Ser Thr Tyr Pro Asp Ser Ile Asn Asn Leu Leu Ile Phe Ser
 20 25 30

agt att att gaa agc tat gaa ggc act gtg aac aaa ttt cgt tgt gga
 Ser Ile Ile Glu Ser Tyr Glu Gly Thr Val Asn Lys Phe Arg Cys Gly
 35 40 45

gat act gta agt ata aag tac gat ata cgt gaa cta aac ggt aat acg 192
 Asp Thr Val Ser Ile Lys Tyr Asp Ile Arg Glu Leu Asn Gly Asn Thr
 50 55 60

ata cta caa gat caa gaa tta aaa ttt act att gga aaa aat gaa gtc
 Ile Leu Gln Asp Gln Glu Leu Lys Phe Thr Ile Gly Lys Asn Glu Val
 65 70 75 80

cct ctt gca ata gag cta ggt gta att aat atg aga caa gac atg gca 288
Pro Leu Ala Ile Glu Leu Gly Val Ile Asn Met Arg Gln Asp Met Ala

85	90	95
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aga cat att att gca cca tta gaa ctt ttg act aat ttt gac aaa cct Arg His Ile Ile Ala Pro Leu Glu Leu Leu Thr Asn Phe Asp Lys Pro 100 105 110	336
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gac aac ttt tga Asp Asn Phe 115	348
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<210> 86 <211> 115 <212> PRT <213> Ehrlichia ruminantium (formerly Cowdria ruminantium) <400> 86	
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Val Asn Ser Thr Tyr Pro Asp Ser Ile Asn Asn Leu Leu Ile Phe Ser 20 25 30	
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Ser Ile Ile Glu Ser Tyr Glu Gly Thr Val Asn Lys Phe Arg Cys Gly 35 40 45	
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Asp Thr Val Ser Ile Lys Tyr Asp Ile Arg Glu Leu Asn Gly Asn Thr 50 55 60	
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Ile Leu Gln Asp Gln Glu Leu Lys Phe Thr Ile Gly Lys Asn Glu Val 65 70 75 80	
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Pro Leu Ala Ile Glu Leu Gly Val Ile Asn Met Arg Gln Asp Met Ala 85 90 95	
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Arg His Ile Ile Ala Pro Leu Glu Leu Leu Thr Asn Phe Asp Lys Pro 100 105 110	
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Asp Asn Phe 115	
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<210> 87 <211> 3829 <212> DNA <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)	
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tttttgttt ataattgaat taaagtgcctt aaagatattt atatagttat tacttagatt 180
attnaattaa attaagctag tgaacaaaga atttgcattt tatataatgg aggtatctat 240
tatcttaca gtttaaataa gaaagcaagg gtttattat tatatagtga atgaaatata 300
ttattactga gtatcatg tttattat acattattca ctattcacaa attcagtgtt 360
tgtgataaac ctaaataatt atacaatat tagggggggg ggggtatat ttttcgtaa 420
gagcttacat taatgttaatt attaatagta tttttgttt taaaagatg taaattctac 480
tgttgggt tactgcataa caatattcag tgataaacaa ggatttacaa taaatacact 540
tgcctttta agaatatttt agtagtttg agaatcatat gatacttgat gatgagtata 600
cctaattgatg agttcggtac ctgtttaca gtttattata ccttacttt ctgcagtaat 660
atgtgctta taaaaaaata gtacattggt gaaaattata tcatttattt ttgttagt 720
atcttttcc attgcgttgg tattgttctc tcaggttat tctgctgatg taatcaaata 780
cagcctaggg ggggggtcg ttccttatgg catagaacctt aaagtgaaca tatttagtgc 840
tactatgctt gtttagtaa atttattgc tgtaatgagt atattgtatg gcatatatcc 900
taacatcaga gaaataggtg ttaacaagat accaagttt tattctgtat tttgctatg 960
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tgagatttcg tctatttctt cttatatttt ggttgcattt gaaaaagata aagctgctt 1080
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tataggctt ttgtatgcata ttactggtac attgaatatt ggagatttgc ttctataat 1200
tcattgataat ttgctggtaa caaatagagt tacacagatt gcaatgtt atattatgg 1260
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 aataccgatg ttaatatgtt ttgttattt taaaagactt ttgaggatgg taggcgtact 3720
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 ctgtataatgc taaccatata tgccataatgc caggaacctt tgttggatc 3829

<210> 88
 <211> 1479
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(1479)
 <223> Corresponds to SEQ ID NO:87, nucleotides 605..2083
 Hypothetical NADH dehydrogenase (ubiquinone)
 Product = "3gdorf1"

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tca tct att gtt gta gta tct ttt tcc att gcg ttg gta ttg ttc Ser Ser Ile Val Val Val Ser Phe Ser Ile Ala Leu Val Leu Phe 35 40 45	144
tct cag gtt tat tct gct gat gta atc aaa tac agc cta ggg ggg tgg Ser Gln Val Tyr Ser Ala Asp Val Ile Lys Tyr Ser Leu Gly Gly Trp 50 55 60	192
gtc gtt cct tat ggc ata gaa ctt aaa gtg aac ata ttt agt gct act Val Val Pro Tyr Gly Ile Glu Leu Lys Val Asn Ile Phe Ser Ala Thr 65 70 75 80	240
atg ctt gtt tta gta aat ttt att gct gta atg agt ata ttg tat ggc	288

Met Leu Val Leu Val Asn Phe Ile Ala Val Met Ser Ile Leu Tyr Gly			
85	90	95	
ata tat cct aac atc aga gaa ata ggt gtt aac aag ata cca agt ttc			336
Ile Tyr Pro Asn Ile Arg Glu Ile Gly Val Asn Lys Ile Pro Ser Phe			
100	105	110	
tat tct gta ttt ttg cta tgt tta ggt ggc ttt ttg ggg ata tta gta			384
Tyr Ser Val Phe Leu Leu Cys Leu Gly Gly Phe Leu Gly Ile Leu Val			
115	120	125	
tca aat gat gtt ttt aat atc tat gtt ttt ctt gag att tcg tct att			432
Ser Asn Asp Val Phe Asn Ile Tyr Val Phe Leu Glu Ile Ser Ser Ile			
130	135	140	
tct tct tat att ttg gtt gca atg gga aaa gat aaa gct gct tta ata			480
Ser Ser Tyr Ile Leu Val Ala Met Gly Lys Asp Lys Ala Ala Leu Ile			
145	150	155	160
gca gca ttt gat tat tta gta att ggt aca att ggg gca act ttt tat			528
Ala Ala Phe Asp Tyr Leu Val Ile Gly Thr Ile Gly Ala Thr Phe Tyr			
165	170	175	
tta ata ggt ata ggc ttt ttg tat gct att act ggt aca ttg aat att			576
Leu Ile Gly Ile Gly Phe Leu Tyr Ala Ile Thr Gly Thr Leu Asn Ile			
180	185	190	
gga gat ttg ttt cta ata att cat gat aat ttg ctg gta aca aat aga			624
Gly Asp Leu Phe Leu Ile Ile His Asp Asn Leu Leu Val Thr Asn Arg			
195	200	205	
gtt aca cag att gca atg tta ttt att atg gta ggt ttg ttt ata aag			672
Val Thr Gln Ile Ala Met Leu Phe Ile Met Val Gly Leu Phe Ile Lys			
210	215	220	
aca gcg cta ttc cca ttt cat aaa tgg tta ata cag gct tat agt ttt			720
Thr Ala Leu Phe Pro Phe His Lys Trp Leu Ile Gln Ala Tyr Ser Phe			
225	230	235	240
gct cct tct ttt att tct gtg ttt tcc ggt act tct act aaa gtt			768
Ala Pro Ser Phe Ile Ser Val Phe Phe Ser Gly Thr Ser Thr Lys Val			
245	250	255	
atg ata tat cta att ata aag atg ata tat gac gtt ttt aaa gct gat			816
Met Ile Tyr Leu Ile Ile Lys Met Ile Tyr Asp Val Phe Lys Ala Asp			
260	265	270	
ttt gtt ttt gtg act tta cct ttt aat att gtt ttt atg tgt ttt gct			864
Phe Val Phe Val Thr Leu Pro Phe Asn Ile Val Phe Met Cys Phe Ala			
275	280	285	
gtg ttg tca ata gtt tgt gga tct tta ctt gca att ttt act agc aat			912
Val Leu Ser Ile Val Cys Gly Ser Leu Leu Ala Ile Phe Thr Ser Asn			
290	295	300	

att aaa aag ata ttt gct tat tca agt att gca cat tta gga tat att Ile Lys Lys Ile Phe Ala Tyr Ser Ser Ile Ala His Leu Gly Tyr Ile 305 310 315 320	960
gta ttt gca gtt agt tta aat act aat tat ggt ttg gtt gca gct ata Val Phe Ala Val Ser Leu Asn Thr Asn Tyr Gly Leu Val Ala Ala Ile 325 330 335	1008
gct tat att att agt cat agc ttg gtt aag tca gca tta ttt atg att Ala Tyr Ile Ser His Ser Leu Val Lys Ser Ala Leu Phe Met Ile 340 345 350	1056
gta ggt agc att gat tat agt tgt ggt aac aga cat ctg aaa gat tgt Val Gly Ser Ile Asp Tyr Ser Cys Gly Asn Arg His Leu Lys Asp Cys 355 360 365	1104
gca aac atg tgg gaa acc atg cca aaa att aca ttg cca ttt att ata Ala Asn Met Trp Glu Thr Met Pro Lys Ile Thr Leu Pro Phe Ile Ile 370 375 380	1152
tta tgt tta agt tta att ggt atg cca gtt act tca ggg ttt att gct Leu Cys Leu Ser Leu Ile Gly Met Pro Val Thr Ser Gly Phe Ile Ala 385 390 395 400	1200
aaa tgg tat att gtt gat gca gtt ata aag tct aat ttt tgg gtt ggt Lys Trp Tyr Ile Val Asp Ala Val Ile Lys Ser Asn Phe Trp Val Gly 405 410 415	1248
att ttt gtg ttg ctt ata ggt tct ggg tta tct ata gtg tat gtt tgg Ile Phe Val Leu Leu Ile Gly Ser Gly Leu Ser Ile Val Tyr Val Trp 420 425 430	1296
aaa ata gtt gaa gca gtg tgt ctt cgt tca cct gat aat aag gta gtt Lys Ile Val Glu Ala Val Cys Leu Arg Ser Pro Asp Asn Lys Val Val 435 440 445	1344
atg tcg tcg ttt gaa aca cca aat gtt atg gta tta tgt att tgg ata Met Ser Ser Phe Glu Thr Pro Asn Val Met Val Leu Cys Ile Trp Ile 450 455 460	1392
atg gta att gct tcg att att gtg gga ata tat cca att cct tta aca Met Val Ile Ala Ser Ile Ile Val Gly Ile Tyr Pro Ile Pro Leu Thr 465 470 475 480	1440
ttg att tct aat aaa ata gcg acg ttg cta tta tat tga Leu Ile Ser Asn Lys Ile Ala Thr Leu Leu Leu Tyr 485 490	1479

<210> 89
 <211> 492
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 89

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20 25 30

Ser Ser Ile Val Val Val Ser Phe Ser Ile Ala Leu Val Leu Phe
35 40 45

Ser Gln Val Tyr Ser Ala Asp Val Ile Lys Tyr Ser Leu Gly Gly Trp
50 55 60

Val Val Pro Tyr Gly Ile Glu Leu Lys Val Asn Ile Phe Ser Ala Thr
65 70 75 80

Met Leu Val Leu Val Asn Phe Ile Ala Val Met Ser Ile Leu Tyr Gly
85 90 95

Ile Tyr Pro Asn Ile Arg Glu Ile Gly Val Asn Lys Ile Pro Ser Phe
100 105 110

Tyr Ser Val Phe Leu Leu Cys Leu Gly Gly Phe Leu Gly Ile Leu Val
115 120 125

Ser Asn Asp Val Phe Asn Ile Tyr Val Phe Leu Glu Ile Ser Ser Ile
130 135 140

Ser Ser Tyr Ile Leu Val Ala Met Gly Lys Asp Lys Ala Ala Leu Ile
145 150 155 160

Ala Ala Phe Asp Tyr Leu Val Ile Gly Thr Ile Gly Ala Thr Phe Tyr
165 170 175

Leu Ile Gly Ile Gly Phe Leu Tyr Ala Ile Thr Gly Thr Leu Asn Ile
180 185 190

Gly Asp Leu Phe Leu Ile Ile His Asp Asn Leu Leu Val Thr Asn Arg
195 200 205

Val Thr Gln Ile Ala Met Leu Phe Ile Met Val Gly Leu Phe Ile Lys
210 215 220

Thr Ala Leu Phe Pro Phe His Lys Trp Leu Ile Gln Ala Tyr Ser Phe
225 230 235 240

Ala Pro Ser Phe Ile Ser Val Phe Phe Ser Gly Thr Ser Thr Lys Val
245 250 255

Met Ile Tyr Leu Ile Ile Lys Met Ile Tyr Asp Val Phe Lys Ala Asp
260 265 270

Phe Val Phe Val Thr Leu Pro Phe Asn Ile Val Phe Met Cys Phe Ala
275 280 285

Val Leu Ser Ile Val Cys Gly Ser Leu Leu Ala Ile Phe Thr Ser Asn
290 295 300

Ile Lys Lys Ile Phe Ala Tyr Ser Ser Ile Ala His Leu Gly Tyr Ile
305 310 315 320

Val Phe Ala Val Ser Leu Asn Thr Asn Tyr Gly Leu Val Ala Ala Ile
325 330 335

Ala Tyr Ile Ile Ser His Ser Leu Val Lys Ser Ala Leu Phe Met Ile
340 345 350

Val Gly Ser Ile Asp Tyr Ser Cys Gly Asn Arg His Leu Lys Asp Cys
355 360 365

Ala Asn Met Trp Glu Thr Met Pro Lys Ile Thr Leu Pro Phe Ile Ile
370 375 380

Leu Cys Leu Ser Leu Ile Gly Met Pro Val Thr Ser Gly Phe Ile Ala
385 390 395 400

Lys Trp Tyr Ile Val Asp Ala Val Ile Lys Ser Asn Phe Trp Val Gly
405 410 415

Ile Phe Val Leu Leu Ile Gly Ser Gly Leu Ser Ile Val Tyr Val Trp
420 425 430

Lys Ile Val Glu Ala Val Cys Leu Arg Ser Pro Asp Asn Lys Val Val

435

440

445

Met Ser Ser Phe Glu Thr Pro Asn Val Met Val Leu Cys Ile Trp Ile
 450 455 460

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 465 470 475 480

Leu Ile Ser Asn Lys Ile Ala Thr Leu Leu Leu Tyr
 485 490

<210> 90
<211> 300
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(300)
<223> Complement to SEQ ID NO:87, nucleotides 2311..2610
Product = "3gdorf2"

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actacctata ttttcttgag tacttacaga tgattgatct ttaggttcaa gctttttctt 180
aagttttta ttgtacttaa agaaataagt actacctata actaatagaa gtatttagtaa 240
cgctattgac tttgggttac taactatata taataataag ttataaaaat cattttagcat 300

<210> 91
<211> 450
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(450)
<223> Complement to SEQ ID NO:87, nucleotides 3209..3658
Hypothetical outer membrane protein, related to proposed ABC tran
sporter
Product = "3gdorf3"

<400> 91
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 aatgtgcttt ttccctaaca tattgctgtt taatatacat gctgaactat ctgaaggtag 180
 taagatattt ttctgtatgc acattgttac tataggagta tagcttcata tcaatgatat 240
 tgaagttact gtaccttattt ttactcctga tattgttact tcatctccta tgtccaaccc 300
 atctacattt gagaaaaatg ctttaactgt ataacaatta cgcaaggtat ttttatatgg 360
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 aaaaatttca ataatatttgc 450

<210> 92
 <211> 226
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 cagcataaaat tcctttcttc acactagcaa tgatttcatt tggatc 226

<210> 93
 <211> 226
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(226)
 <223> Complement to SEQ ID NO:92, nucleotides <1..>226
 Hypothetical tldD protein
 Product = "4gdorfli"

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 cagaagctga aaaaacaaat ttaccagatg taatatctac ctgaccacca gcaaaattca 180
 cagcataaaat tcctttcttc acactagcaa tgatttcatt tggatc 226

<210> 94

<211> 160
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 94
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gagcagcccg gcgtggccga gctgggcgac gccgtcgggc gtgcacagcg tgcccatatg 120
cgccgtgatc ggcaggccgt gggcgccggc gaactcgatc 160

<210> 95
<211> 299
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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tagtaaaca aaaaatattt acccaaaaca agtaaatatc aatactatca actcagttact 180
accacctaattt agtaaccacc aaggcattgc tttacaagtt tcaatagtag atacagtaag 240
catagaagac gtattatcta atattcctac agagatttca acaataatac ttttagatc 299

<210> 96
<211> 297
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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<223> Corresponds to SEQ ID NO:95, nucleotides <1..>297
Product = "6gdorfli"

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1 5 10 15

aaa tgt cat gag ctt tta gtt aca gaa aat ttc att aaa cat aac aat 96
Lys Cys His Glu Leu Leu Val Thr Glu Asn Phe Ile Lys His Asn Asn
20 25 30

gga ata caa aaa att aga gag ctt agt aaa caa aaa aat att tac cca 144
Gly Ile Gln Lys Ile Arg Glu Leu Ser Lys Gln Lys Asn Ile Tyr Pro
35 40 45

aaa caa gta aat atc aat act atc aac tca gta cta cca cct aat agt 192

Lys Gln Val Asn Ile Asn Thr Ile Asn Ser Val Leu Pro Pro Asn Ser			
50	55	60	
aac cac caa ggc att gct tta caa gtt tca ata gta gat aca gta agc			240
Asn His Gln Gly Ile Ala Leu Gln Val Ser Ile Val Asp Thr Val Ser			
65	70	75	80
ata gaa gac gta tta tct aat att cct aca gag att tca aca ata ata			288
Ile Glu Asp Val Leu Ser Asn Ile Pro Thr Glu Ile Ser Thr Ile Ile			
85	90	95	
ctt tta gat			297
Leu Leu Asp			

#

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<211>	99		
<212>	PRT		
<213>	Ehrlichia ruminantium (formerly Cowdria ruminantium)		

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Lys Cys His Glu Leu Leu Val Thr Glu Asn Phe Ile Lys His Asn Asn			
20	25	30	

Gly Ile Gln Lys Ile Arg Glu Leu Ser Lys Gln Lys Asn Ile Tyr Pro			
35	40	45	

Lys Gln Val Asn Ile Asn Thr Ile Asn Ser Val Leu Pro Pro Asn Ser			
50	55	60	

Asn His Gln Gly Ile Ala Leu Gln Val Ser Ile Val Asp Thr Val Ser			
65	70	75	80

Ile Glu Asp Val Leu Ser Asn Ile Pro Thr Glu Ile Ser Thr Ile Ile			
85	90	95	

Leu Leu Asp

<210>	98		
<211>	2104		
<212>	DNA		
<213>	Ehrlichia ruminantium (formerly Cowdria ruminantium)		

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cattttacca gaatgatgaa taatgacatt tcataaagtt taataaataa ggatttataa	180
tgaatgctaa agaaaaaaat attagagaag aaattttaaa tcttcaaaaa aagattgctg	240
aatgagacaa tgcttattat aatttggata atcctattgt aactgatgaa atttatgata	300
ctgagtttat tagacttcaa aaatttagaaa aacaatatacg tcatttgcta acttatgaa	360
aagttaaaaa ctctccaacg caaaaaatttgc atgcaaagtc tttatcaata ttgataaaag	420
taattcataa aaaaccaatg ctttctttaa acaaagcata ttcaattgaa gaaattaaga	480
aatttattaa aaagattgaa aaatatacta atgattttc attttttattt gaacctaaaa	540
ttgatggct ttcttatttca ttaactttagt aaaatggaaa actaattttaga ggtgtaacta	600
gaggagatgg aataacagga gaagatgtt caaaaaatatt tttacaaattt aatgatatcc	660
ctaaagaaat agaatacataa cacaaaatcg aattaagagg aaaaatataat ttatctattt	720
ctagatttaa tgaattaaat gaagaaaattt taaaaataa tttaccgcct ttagctaacc	780
caagaaatgc agcagccgga actttaagac aatttagattc taatattgtt tctcaaagag	840
ggttgtcatc ttttatatat ttttagtgc atgctccag tcataatattt tggacaatgg	900
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ctaaaaatataat taatcaaattt gaagaatata taaataattt tccagaactt aaaaaaacat	1020
ttgattttga agcagatggt gtagtttata aattaaatgt aattaaatgt tgaaataaaaa	1080
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aaattacaac aattaaaaaaat atatttataa ctattggaa aactggccta gtcacttata	1200
atggccaagt taaaactgtc gaaatttctg gttccaaaat aaactttgc acattaaata	1260
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atgaaaataa attaatttctt agtccacttag atttttataa tttaaaaaat aataaaaaatgt	1620

aactaacaca attagaaaaa ttaggaacta aatctataat gaaaatttttta gattcaattg 1680
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 ttgattttga ttctttaatt caatataatg aaattggcc AAAAATTATT gattcagtta 1860
 AAAAATGACT atcagctgaa aataataaaa aattaattaa tgactttctt aatagaggaa 1920
 tgaatttcga acatatttca aatataaaaa gcaaattatt agatgaaatt aatattgtta 1980
 ttacaggaac attatctaag cctagaaattt attttgaaga attaataaaa gcaaataacg 2040
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 gatc 2104

<210> 99
<211> 642
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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<222> (1)...(642)
<223> Corresponds to SEQ ID NO:98, nucleotides 180..>2104
 Hypothetical DNA ligase
 Product = "7gdorfli"

<400> 99

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Ile Val Thr Asp Glu Ile Tyr Asp Thr Glu Phe Ile Arg Leu Gln Lys
 35 40 45

Leu Glu Lys Gln Tyr Ser His Leu Leu Thr Tyr Glu Glu Val Lys Asn
 50 55 60

Ser Pro Thr Gln Lys Ile Asp Ala Lys Ser Leu Ser Ile Phe Asp Lys
 65 70 75 80

Val Ile His Lys Lys Pro Met Leu Ser Leu Asn Lys Ala Tyr Ser Ile
85 90 95

Glu Glu Ile Lys Lys Phe Ile Lys Lys Ile Glu Lys Tyr Thr Asn Asp
100 105 110

Phe Ser Phe Phe Ile Glu Pro Lys Ile Asp Gly Leu Ser Ile Ser Leu
115 120 125

Thr Tyr Glu Asn Gly Lys Leu Ile Arg Gly Val Thr Arg Gly Asp Gly
130 135 140

Ile Thr Gly Glu Asp Val Thr Lys Asn Ile Leu Gln Ile Asn Asp Ile
145 150 155 160

Pro Lys Glu Ile Glu Tyr Lys His Lys Ile Glu Leu Arg Gly Lys Ile
165 170 175

Tyr Leu Ser Ile Ser Arg Phe Asn Glu Leu Asn Glu Glu Asn Leu Lys
180 185 190

Asn Asn Leu Pro Pro Leu Ala Asn Pro Arg Asn Ala Ala Gly Thr
195 200 205

Leu Arg Gln Leu Asp Ser Asn Ile Val Ser Gln Arg Gly Leu Ser Ser
210 215 220

Phe Ile Tyr Phe Val Val Asp Ala Pro Ser His Asn Ile Trp Thr Met
225 230 235 240

Glu Asp Ala Phe Cys Phe Leu Lys Lys Asn Asn Phe His Val Val Lys
245 250 255

Asp Tyr Lys Leu Ala Lys Asn Ile Asn Gln Ile Glu Glu Tyr Ile Asn
260 265 270

Asn Phe Pro Glu Leu Lys Lys Thr Phe Asp Phe Glu Ala Asp Gly Val
275 280 285

Val Ile Lys Leu Asn Glu Ile Lys Trp Trp Asn Lys Ile Gly Gln Thr
290 295 300

Gln Lys Phe Pro His Tyr Ala Ile Ala Phe Lys Phe Glu Pro Asn Ile
305 310 315 320

Glu Ile Thr Thr Ile Lys Lys Ile Phe Ile Thr Ile Gly Arg Thr Gly
325 330 335

Leu Val Thr Tyr Asn Gly Gln Val Lys Thr Val Glu Ile Ser Gly Ser
340 345 350

Lys Ile Asn Phe Ala Thr Leu Asn Asn Phe Asn Tyr Val Lys Glu Leu
355 360 365

Asn Leu Asn Val Gly Asp Glu Val Tyr Ile Lys Lys Ala Gly Glu Ile
370 375 380

Ile Pro Cys Ile Ile Gly Leu Val Asn Pro Lys Gly Lys Pro Asp Tyr
385 390 395 400

Phe Lys Arg Ile Glu Thr Cys Pro Tyr Cys Asn Ser Lys Leu Ile Glu
405 410 415

Ser Glu Thr Phe Leu Glu Glu Tyr Cys Glu Asn Tyr Asn Cys Pro Glu
420 425 430

Ile Ile Lys Lys Gln Leu Ile His Phe Ser Ser Lys Glu Cys Met Asn
435 440 445

Phe Phe Ser Met Gly Glu Lys Ile Val Glu Lys Leu Tyr Glu Asn Lys
450 455 460

Leu Ile Leu Ser Pro Leu Asp Phe Tyr Asn Leu Lys Asn Asn Lys Asn
465 470 475 480

Glu Leu Thr Gln Leu Glu Lys Leu Gly Thr Lys Ser Ile Met Lys Ile
485 490 495

Leu Asp Ser Ile Glu Asp Ser Lys Lys Leu Gly Leu Asp Lys Phe Ile
500 505 510

Phe Ala Leu Ser Ile Lys His Ile Gly Gln Lys Val Ala Ser Phe Ile
515 520 525

Thr Ser Lys Val Gln Lys Leu Ser Glu Phe Leu Thr Phe Asp Phe Asp
 530 535 540

Ser Leu Ile Gln Tyr Asn Glu Ile Gly Pro Lys Ile Ile Asp Ser Val
 545 550 555 560

Lys Lys Trp Leu Ser Ala Glu Asn Asn Lys Lys Leu Ile Asn Asp Phe
 565 570 575

Leu Asn Arg Gly Met Asn Phe Glu His Ile Ser Asn Ile Lys Ser Lys
 580 585 590

Leu Leu Asp Gly Ile Asn Ile Val Ile Thr Gly Thr Leu Ser Lys Pro
 595 600 605

Arg Asn Tyr Phe Glu Glu Leu Ile Lys Ala Asn Asn Gly Asn Ile Val
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 625 630 635 640

Gly Ser

<210> 100
<211> 4055
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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accatatctat ccacatttct atttgcttac gcataactg tggataccaa ttaatcttac			180
ggacctgttc taatagctca tcttttatct ctacaacctt aataaaccat tggttactta			240
acaatatttc aataggcatt cctgatcgct cagcacattt cacattgtgt aatatttcct			300
cttttttat cagtaaatta catttactta aggtttcaag taccagctt cttgcttcta			360
ctattgatac tccatgtaat ttaccagata aagtatctgt ctctgcaatg ttatgtttaa			420
gatcaagagt acctgatttta cttattataa tctgcgtatt taaattatgt ttattccacc			480

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<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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1 5 10 15		
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Leu Phe Glu Tyr His Thr Gly Asn Gly Ile Pro Lys Tyr Leu Cys Arg		
20 25 30		
gat atg cac cag tcc cag ttt aac cca tct atc cac att tct att tgc		144
Asp Met His Gln Ser Gln Phe Asn Pro Ser Ile His Ile Ser Ile Cys		
35 40 45		
tta cgc ata gac tgt gga tac caa tta atc tta cgg acc tgt tct aat		192
Leu Arg Ile Asp Cys Gly Tyr Gln Leu Ile Leu Arg Thr Cys Ser Asn		
50 55 60		
agc tca tct ttt atc tct aca acc tta ata aac cat tgg tta ctt aac		240
Ser Ser Ser Phe Ile Ser Thr Leu Ile Asn His Trp Leu Leu Asn		
65 70 75 80		
aat att tca ata ggc att cct gat cgc tca gca cat ttc aca ttg tgt		288
Asn Ile Ser Ile Gly Ile Pro Asp Arg Ser Ala His Phe Thr Leu Cys		
85 90 95		
aat att tcc tct ttt atc agt aaa tta cat tta ctt aag gtt tca		336
Asn Ile Ser Ser Phe Phe Ile Ser Lys Leu His Leu Leu Lys Val Ser		
100 105 110		
agt acc agc ttt ctt gct tct act att gat act cca tgt aat tta cca		384
Ser Thr Ser Phe Leu Ala Ser Thr Ile Asp Thr Pro Cys Asn Leu Pro		

115	120	125	
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150	155	160	480
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165	170	175	528
tct att ttt act tgt tca tct gat aaa atc ggt act tta ttc Ser Ile Phe Thr Cys Ser Ser Asp Lys Ile Gly Thr Leu Phe			
180	185	190	576
ata ggt act ata gca tac tga Ile Gly Thr Ile Ala Tyr			
195	200		603
102			
200			
PRT			
Ehrlichia ruminantium (formerly Cowdria ruminantium)			
102			
Gly Ser Ser Phe Thr Ser Gly Ile Ile Ile Ser Ser Leu Ser			
5	10	15	
Glu Tyr His Thr Gly Asn Gly Ile Pro Lys Tyr Leu Cys Arg			
20	25	30	
His Gln Ser Gln Phe Asn Pro Ser Ile His Ile Ser Ile Cys			
35	40	45	
Ile Asp Cys Gly Tyr Gln Leu Ile Leu Arg Thr Cys Ser Asn			
55	60		
Ser Phe Ile Ser Thr Thr Leu Ile Asn His Trp Leu Leu Asn			
70	75	80	
Ser Ile Gly Ile Pro Asp Arg Ser Ala His Phe Thr Leu Cys			
85	90	95	
Ser Ser Phe Phe Ile Ser Lys Leu His Leu Leu Lys Val Ser			

100

105

110

Ser Thr Ser Phe Leu Ala Ser Thr Ile Asp Thr Pro Cys Asn Leu Pro
 115 120 125

Asp Lys Val Ser Val Ser Ala Met Leu Cys Leu Arg Ser Arg Val Pro
 130 135 140

Asp Leu Leu Ile Ile Ile Cys Val Phe Lys Leu Cys Leu Phe His Gln
 145 150 155 160

Tyr Thr Ser Asn Ser Ser Pro Asn Val Gln His Ile Thr Arg Pro Val
 165 170 175

Pro Leu Ser Ile Phe Thr Cys Ser Ser Asp Lys Ile Gly Thr Leu Phe
 180 185 190

Pro Asn Ile Gly Thr Ile Ala Tyr
 195 200

<210> 103
<211> 1321
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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<222> (1)..(1321)
<223> n = a, c, g, or t

<220>
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<223> Complement to SEQ ID NO:100, nucleotides <1..1321
Hypothetical valine-tRNA ligase
Product = "3hworfli"

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cggacctgtt ctaatagctc atctttatc tctacaacct taataaacca ttggttactt 240

aacaatattt caataggcat tcctgatcgc tcagcacatt tcacattgtg taatattcc	300
tctttttta tcagtaaatt acatttactt aaggttcaa gtaccagctt tcttgcttct	360
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agatcaagag tacctgattt acttattata atctgcgtat ttaaattatg tttattccac	480
caatatacat ctaattcatc accaaatgta caacacatta caagaccagt acccttatct	540
attttactt gttcatctga taaaatcggt actttattcc caaatatagg tactatagca	600
tactgacctt gaagatgctg atatcttata tccaatggat taaaaataaa agcaacacaa	660
gctggcatta attctggacg cgtcgttgca atatttatta gctctccagc ctccgtagaa	720
aaggctatcg tactcataaa cgatgacatt tcctttcct caacctcaac tctcgctatc	780
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tattccagat cccaatcata actaatacca agagattgaa acaatatttt aaattccatt	960
ctgaattttg cagatacttc attacataat gccttaaatt ctttacgatc aatatctgtc	1020
gcacgtactt ttttatctt ttcaactaaa cgttctgttgc gcaatccatt gtcatcaaat	1080
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tgacagtagc taaaaacatg tcctatatgt agttgtcctg atattgttgg aggaggagta	1200
tcaataataa actgtttatc ttgttaaattc ttccatttat ataattttat tttatccaa	1260
taggtattaa gtttttcttc tgtatcttg aacttgtatt tattactaaa aagagactgc	1320
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<210> 104
 <211> 549
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(549)
 <223> Complement to SEQ ID NO:100, nucleotides 3508..>4055
 Hypothetical glutamate-cysteine ligase
 Product = "3hworf3i"

<400> 104
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acagaatatt ttaccttctt gctctctaaa acttacatct acaaaatcac aacctacaga	120
attaggtta gagaatttat cttaacagt attataccta tataaataac acgaaggagt	180
atcacctatg aaatatacta atggttctgc agtataacca ttaaacaact cttcagtcat	240
tataccttct tgtattatta cacgctcaac tatccctta tccttaattc ttttcatctt	300
attgcgattt ttttattta acttcaatat gtcacccacca caatatgcta caataattcc	360
cattccatat gttccattat ctgttttac aaacacatac ggttgttctg taatactgta	420
taattgaaat ttattacgta tttcttgaat cataacatca actttatcag caatgtgttc	480
tactccataa ttactaaaaa aacagatgtt atcacaacta gaaaataatg tagaaatcaa	540
ccaaggatc	549

<210> 105
 <211> 4122
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 105	
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agctcctacc gttttattat ggtgatactt tccttcaatt tttcctactg caccattaaa	120
aaatatctct ctcataattt aacttcctta aaaattgagt aaaccttcac ctcataata	180
atacaaaaaa gtttaactta ataaagtatt tttaacaagt gtattattaa ttacaccctc	240
aaaagcgcta tagtttgct ttcattttt taaaaaaaaat taaagttgca atttaatac	300
atatttaaca ataaatattt ttacttatct catttaagaa aaaacctact tgacacaagg	360
tatattaatg atacattatc aagttgttga taatataaaa atgatctatt caattaaaaa	420
tactaaaaaa ggcccataat taacgtgtgg atatttatat gttgatcaca gctaggctac	480
gttatgctat aatgtttatg gtaaaaattgg ctcatggctt ttgcacgcaa caaaataagt	540
tgcaaccagt aagaatgtca tatattgcaa gtaatcaatc tttatctgaa ggatatctt	600
aacaggtaat tgttcaatta aagaaaaaag ggcttattaa tgctacaaaaa ggtccaggtg	660
gtggttattt actaagtatt gtccttcatt taattacact tagtcttata cttgaatcaa	720
taggcgaaaa tattaaaattt acaagatgcg aaaataacag tccaggttgt ctatcgaata	780
ataatagatg tgtaactcac aaattatggg atgatataagg aaatttatata aaagattatt	840
taaataataat ttcacttagag gatatactaa ataataattt tagtcaaac atagcactac	900

ataaaaacga ggaaccctat atatatgctg attacaattc aacatctacg atactacctg	960
aagtaaaata tcaattgaat aatttatcct atataaaatt atataatcca tcttcaatac	1020
ataaaactagg tcaaaaaaca aaaagtataa tagaagaaac aagaaacata gctattaagc	1080
aactaaatgc acaatattat gatgttagttt ttacatcctc tggtagacaa gcaaacaatt	1140
tagtcataa tagtacatca gactataaac atttaatttc ttctacagaa catctatcta	1200
ttataaaatg tgctactaat gcagaattaa tacctgttga ttctaatggc ataatatgtc	1260
taaatgcatt gagtagtctt ttacataagt taaaagatga caaaatacta gtatcagtaa	1320
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ataaatttgg agcatttagta cacacagatg ccataacaagc gtgtggaaaa atccatata	1440
atattgaaga ttttaggagtt gatttgttac caatatcatc acataaactt ggcagcattt	1500
ctggagcagg agtgttattc tttaatagca aaaagataaa tataaaaccc atgataattt	1560
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taagaaataa attggaaaaat gaaatattat cttagttcc taacgctcaa atatttagta	1740
gaaatgtcga gagactacca aatactagtt gtatttcaat gccaaatgta aatagtgaga	1800
ttcaagtaat aagcttgac ataaaaata ttgcagtagg taacgggtca gcatgttcca	1860
caggagtagt agaaccctct catgtgttat ctgcaatggg ggtaaatcag gagattgcaa	1920
ataattcaat aaggatttagc ttaagtcctg acactacaga tgagcatata agaactata	1980
taaactgttg gtacgaaata tatacacata atcaagtgc taaatgaaat taggtgtaaa	2040
atgatgcaaa aattagaaga ttactatatc attaacgata tcaaaaatag gttataacat	2100
ggaaaaataa aaagatatac aacgacatata taatctaccc atatttctt attatcaatc	2160
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taatcctcat tcacgtatgc attgtttgg atggaaagct gagtcggctg ttgaatttagc	2280
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tgctacagaa tcaaataatt tggcaattaa aggtgtacca aactttataa aaagtaaagg	2400
aaatcacatt attacagtac gtacagagca taaatgtgtt ttagattcat gtcgccattt	2460
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taatttatta aaatcagcta taactgataa gactatattt gatcggtta tggtaaa	2580

caatgaaatt ggtgtcattc aaccaataga ggaaatagga aaaatttgcataatcatgg 2640
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aatgaatata gatttgctta gtatatcagg acataaaata tatgctccaa tggaaatagg 2760
ggcattatat gtacgtaaac gtcaaccaag aatacgactt actcctataa taaatggtgg 2820
tggacaagaa cgtggtatga gatctggaac catabctact ccattagcag taggtttagg 2880
ggaagcagca tatatagctc aggaagtaat ggaagatgaa gccatttagga taaaagaatt 2940
gcgtgatatt ttatatagtg aaataaaaaa acatttaccc tatgtaatac tgaatggtga 3000
ttatgaacaa cgtatagcag gaaatttaaa tttaagttt ccatatgttag aaggagaatc 3060
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tattagattt ggaataggta ggttactac aaaagcagaa attttatatg cagcggatct 3240
tattgtaaat agcataaaaga ggttgcgtga gatgagtcct ttatggaaa tggtaacaaga 3300
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cagctataaa tgactatcat atgaaacaag caaacaaaaa aaatgctact aaagatccta 3780
atgaataata cagcaataat atgcaatcag gtttatctat ggataaagaa gtgttgatac 3840
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ttgataagaa aaaagattct gtcattggga ttagaataat ggtagcgcaa aaaggatgtt 4020
ttggttttaa gtataatata gaatatgcat atgatataa aatgttagat gtacaattc 4080
aagtaaaata tcaaaatcaa aattttataa ttttgattga tc 4122

<211> 1569
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1) .. (1569)
<223> Corresponds to SEQ ID NO:105, nucleotides 459..2027
Hypothetical iron-sulfur co-factor synthesis
Product = "11hworf1"

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1 5 10 15		
ttg gct cat ggt ctt tgc acg caa caa aat aag ttg caa cca gta aga		96
Leu Ala His Gly Leu Cys Thr Gln Gln Asn Lys Leu Gln Pro Val Arg		
20 25 30		
atg tca tat att gca agt aat caa tct tta tct gaa gga tat ctt gaa		144
Met Ser Tyr Ile Ala Ser Asn Gln Ser Leu Ser Glu Gly Tyr Leu Glu		
35 40 45		
cag gta att gtt caa tta aag aaa aaa ggg ctt att aat gct aca aaa		192
Gln Val Ile Val Gln Leu Lys Lys Lys Gly Leu Ile Asn Ala Thr Lys		
50 55 60		
ggt cca ggt ggt tat tca cta agt att gct cct cat tta att aca		240
Gly Pro Gly Gly Tyr Ser Leu Ser Ile Ala Pro His Leu Ile Thr		
65 70 75 80		
ctt agt ctt ata ctt gaa tca ata ggc gaa aat att aaa att aca aga		288
Leu Ser Leu Ile Leu Glu Ser Ile Gly Glu Asn Ile Lys Ile Thr Arg		
85 90 95		
tgc gaa aat aac agt cca ggt tgt cta tcg aat aat aat aga tgt gta		336
Cys Glu Asn Asn Ser Pro Gly Cys Leu Ser Asn Asn Asn Arg Cys Val		
100 105 110		
act cac aaa tta tgg gat gat ata gga aat tat ata aaa gat tat tta		384
Thr His Lys Leu Trp Asp Asp Ile Gly Asn Tyr Ile Lys Asp Tyr Leu		
115 120 125		
aat aat att tca cta gag gat ata gta aat aat aat ttt agg tca aac		432
Asn Asn Ile Ser Leu Glu Asp Ile Val Asn Asn Asn Phe Arg Ser Asn		
130 135 140		
ata gca cta cat aaa aac gag gaa ccc tat ata tat gct gat tac aat		480
Ile Ala Leu His Lys Asn Glu Glu Pro Tyr Ile Tyr Ala Asp Tyr Asn		
145 150 155 160		
tca aca tct acg ata cta cct gaa gta aaa tat caa ttg aat aat tta		528
Ser Thr Ser Thr Ile Leu Pro Glu Val Lys Tyr Gln Leu Asn Asn Leu		

165

170

175

tcc tat ata aaa tta tat aat cca tct tca ata cat aaa cta ggt caa Ser Tyr Ile Lys Leu Tyr Asn Pro Ser Ser Ile His Lys Leu Gly Gln 180	185	190	576	
aaa aca aaa agt ata ata gaa gaa aca aga aac ata gct att aag caa Lys Thr Lys Ser Ile Ile Glu Glu Thr Arg Asn Ile Ala Ile Lys Gln 195	200	205	624	
cta aat gca caa tat tat gat gta gtt ttt aca tcc tct ggt aca gaa Leu Asn Ala Gln Tyr Tyr Asp Val Val Phe Thr Ser Ser Gly Thr Glu 210	215	220	672	
gca aac aat tta gtc atc aat agt aca tca gac tat aaa cat tta att Ala Asn Asn Leu Val Ile Asn Ser Thr Ser Asp Tyr Lys His Leu Ile 225	230	235	240	720
tct tct aca gaa cat cta tct att ata aaa tgt gct act aat gca gaa Ser Ser Thr Glu His Leu Ser Ile Ile Lys Cys Ala Thr Asn Ala Glu 245	250	255	768	
tta ata cct gtt gat tct aat gga ata ata tgt cta aat gca ttg agt Leu Ile Pro Val Asp Ser Asn Gly Ile Ile Cys Leu Asn Ala Leu Ser 260	265	270	816	
agt ctt tta cat aag ttt aaa gat gac aaa ata cta gta tca gta atg Ser Leu Leu His Lys Phe Lys Asp Asp Lys Ile Leu Val Ser Val Met 275	280	285	864	
aca gca aac aat gaa act ggt gct att caa cca ata aaa aaa atc gta Thr Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Ile Lys Lys Ile Val 290	295	300	912	
gaa cta tca cat aaa ttt gga gca tta gta cac aca gat gcc ata caa Glu Leu Ser His Lys Phe Gly Ala Leu Val His Thr Asp Ala Ile Gln 305	310	315	320	960
gcg tgt gga aaa atc cat ata gat att gaa gat tta gga gtt gat ttg Ala Cys Gly Ile His Ile Asp Ile Glu Asp Leu Gly Val Asp Leu 325	330	335	1008	
tta aca ata tca tca cat aaa ctt ggc agc att gct gga gca gga gtg Leu Thr Ile Ser Ser His Lys Leu Gly Ser Ile Ala Gly Ala Gly Val 340	345	350	1056	
tta ttc ttt aat agc aaa aag ata aat ata aaa cct atg ata att ggt Leu Phe Phe Asn Ser Lys Lys Ile Asn Ile Lys Pro Met Ile Ile Gly 355	360	365	1104	
gga cat caa gag aaa gga tta aga gca gga act gaa aat gtt tta gcg Gly His Gln Glu Lys Gly Leu Arg Ala Gly Thr Glu Asn Val Leu Ala 370	375	380	1152	
ata tac tta tta tct ata tca ctt agt aat tta tat aaa tct ata aca			1200	

Ile Tyr Leu Leu Ser Ile Ser Leu Ser Asn Leu Tyr Lys Ser Ile Thr			
385	390	395	400
aag atg ctt ctt gtt gaa aaa tta aga aat aaa ttg gaa aat gaa ata			1248
Lys Met Leu Leu Val Glu Lys Leu Arg Asn Lys Leu Glu Asn Glu Ile			
405	410	415	
tta tct tta gtt cct aac gct caa ata ttt agt aga aat gtc gag aga			1296
Leu Ser Leu Val Pro Asn Ala Gln Ile Phe Ser Arg Asn Val Glu Arg			
420	425	430	
cta cca aat act agt tgt att tca atg cca aat gta aat agt gag att			1344
Leu Pro Asn Thr Ser Cys Ile Ser Met Pro Asn Val Asn Ser Glu Ile			
435	440	445	
caa gta ata agc ttt gac ata aaa aat att gca gta ggt aac ggg tca			1392
Gln Val Ile Ser Phe Asp Ile Lys Asn Ile Ala Val Gly Asn Gly Ser			
450	455	460	
gca tgt tcc aca gga gta gta gaa ccc tct cat gtg tta tct gca atg			1440
Ala Cys Ser Thr Gly Val Val Glu Pro Ser His Val Leu Ser Ala Met			
465	470	475	480
ggg gta aat cag gag att gca aat aat tca ata agg att agc tta agt			1488
Gly Val Asn Gln Glu Ile Ala Asn Ser Ile Arg Ile Ser Leu Ser			
485	490	495	
cct gac act aca gat gag cat ata aga act ata gta aac tgt tgg tac			1536
Pro Asp Thr Thr Asp Glu His Ile Arg Thr Ile Val Asn Cys Trp Tyr			
500	505	510	
gaa ata tat aca cat aat caa gtg cat aaa tga			1569
Glu Ile Tyr Thr His Asn Gln Val His Lys			
515	520		
<210> 107			
<211> 522			
<212> PRT			
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)			
<400> 107			
Met Leu Ile Thr Ala Arg Leu Arg Tyr Ala Ile Met Phe Met Val Lys			
1	5	10	15
Leu Ala His Gly Leu Cys Thr Gln Gln Asn Lys Leu Gln Pro Val Arg			
20	25	30	
Met Ser Tyr Ile Ala Ser Asn Gln Ser Leu Ser Glu Gly Tyr Leu Glu			
35	40	45	

Gln Val Ile Val Gln Leu Lys Lys Gly Leu Ile Asn Ala Thr Lys
50 55 60

Gly Pro Gly Gly Tyr Ser Leu Ser Ile Ala Pro His Leu Ile Thr
65 70 75 80

Leu Ser Leu Ile Leu Glu Ser Ile Gly Glu Asn Ile Lys Ile Thr Arg
85 90 95

Cys Glu Asn Asn Ser Pro Gly Cys Leu Ser Asn Asn Asn Arg Cys Val
100 105 110

Thr His Lys Leu Trp Asp Asp Ile Gly Asn Tyr Ile Lys Asp Tyr Leu
115 120 125

Asn Asn Ile Ser Leu Glu Asp Ile Val Asn Asn Asn Phe Arg Ser Asn
130 135 140

Ile Ala Leu His Lys Asn Glu Glu Pro Tyr Ile Tyr Ala Asp Tyr Asn
145 150 155 160

Ser Thr Ser Thr Ile Leu Pro Glu Val Lys Tyr Gln Leu Asn Asn Leu
165 170 175

Ser Tyr Ile Lys Leu Tyr Asn Pro Ser Ser Ile His Lys Leu Gly Gln
180 185 190

Lys Thr Lys Ser Ile Ile Glu Glu Thr Arg Asn Ile Ala Ile Lys Gln
195 200 205

Leu Asn Ala Gln Tyr Tyr Asp Val Val Phe Thr Ser Ser Gly Thr Glu
210 215 220

Ala Asn Asn Leu Val Ile Asn Ser Thr Ser Asp Tyr Lys His Leu Ile
225 230 235 240

Ser Ser Thr Glu His Leu Ser Ile Ile Lys Cys Ala Thr Asn Ala Glu
245 250 255

Leu Ile Pro Val Asp Ser Asn Gly Ile Ile Cys Leu Asn Ala Leu Ser
260 265 270

Ser Leu Leu His Lys Phe Lys Asp Asp Lys Ile Leu Val Ser Val Met
275 280 285

Thr Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Ile Lys Lys Ile Val
290 295 300

Glu Leu Ser His Lys Phe Gly Ala Leu Val His Thr Asp Ala Ile Gln
305 310 315 320

Ala Cys Gly Lys Ile His Ile Asp Ile Glu Asp Leu Gly Val Asp Leu
325 330 335

Leu Thr Ile Ser Ser His Lys Leu Gly Ser Ile Ala Gly Ala Gly Val
340 345 350

Leu Phe Phe Asn Ser Lys Lys Ile Asn Ile Lys Pro Met Ile Ile Gly
355 360 365

Gly His Gln Glu Lys Gly Leu Arg Ala Gly Thr Glu Asn Val Leu Ala
370 375 380

Ile Tyr Leu Leu Ser Ile Ser Leu Ser Asn Leu Tyr Lys Ser Ile Thr
385 390 395 400

Lys Met Leu Leu Val Glu Lys Leu Arg Asn Lys Leu Glu Asn Glu Ile
405 410 415

Leu Ser Leu Val Pro Asn Ala Gln Ile Phe Ser Arg Asn Val Glu Arg
420 425 430

Leu Pro Asn Thr Ser Cys Ile Ser Met Pro Asn Val Asn Ser Glu Ile
435 440 445

Gln Val Ile Ser Phe Asp Ile Lys Asn Ile Ala Val Gly Asn Gly Ser
450 455 460

Ala Cys Ser Thr Gly Val Val Glu Pro Ser His Val Leu Ser Ala Met
465 470 475 480

Gly Val Asn Gln Glu Ile Ala Asn Asn Ser Ile Arg Ile Ser Leu Ser
485 490 495

Pro Asp Thr Thr Asp Glu His Ile Arg Thr Ile Val Asn Cys Trp Tyr
500 505 510

Glu Ile Tyr Thr His Asn Gln Val His Lys
515 520

<210> 108
<211> 1242
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<220>
<221> CDS
<222> (1)..(1242)
<223> Corresponds to SEQ ID NO:105, nucleotides 2099..3340
Hypothetical iron-sulfur co-factor synthesis
Product = "11hworf2"

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1 5 10 15

ctt gat tat caa tcc aca act aaa acg gat agt aga gtc tta gat gct 96
 Leu Asp Tyr Gln Ser Thr Thr Lys Thr Asp Ser Arg Val Leu Asp Ala
 20 25 30

atg att cca tat ttt caa gag ttt tct aat cct cat tca cgt agt cat 144
 Met Ile Pro Tyr Phe Gln Glu Phe Ser Asn Pro His Ser Arg Ser His
 35 40 45

tgt ttt gga tgg aaa gct gag tcg gct gtt gaa tta gca cga gaa aga	192
Cys Phe Gly Trp Lys Ala Glu Ser Ala Val Glu Leu Ala Arg Glu Arg	
50 55 60	

att gca tct tta ata aat gct gaa agt aaa gaa gta ata ttc act tct 240
 Ile Ala Ser Leu Ile Asn Ala Glu Ser Lys Glu Val Ile Phe Thr Ser
 65 70 75 80

ggt gct aca gaa tca aat aat ttg gca att aaa ggt gta gca aac ttt 288
Gly Ala Thr Glu Ser Asn Asn Leu Ala Ile Lys Gly Val Ala Asn Phe
85 90 95

tat aaa agt aaa gga aat cac att att aca gta cgt aca gag cat aaa 336
Tyr Lys Ser Lys Gly Asn His Ile Ile Thr Val Arg Thr Glu His Lys
100 105 110

act tac tta gat gta caa aaa aat ggt att tta gat ctt aat tta tta	432		
Thr Tyr Leu Asp Val Gln Lys Asn Gly Ile Leu Asp Leu Asn Leu Leu			
130	135	140	
aaa tca gct ata act gat aag act ata ttg gta tcg gtt atg atg gta	480		
Lys Ser Ala Ile Thr Asp Lys Thr Ile Leu Val Ser Val Met Met Val			
145	150	155	160
aac aat gaa att ggt gtc att caa cca ata gag gaa ata gga aaa att	528		
Asn Asn Glu Ile Gly Val Ile Gln Pro Ile Glu Glu Ile Gly Lys Ile			
165	170	175	
tgt cat aat cat gga gta ttc ttt cat act gat gca gct caa gca ttt	576		
Cys His Asn His Gly Val Phe Phe His Thr Asp Ala Ala Gln Ala Phe			
180	185	190	
ggg aaa ata cca ata gat gta aac aaa atg aat ata gat ttg ctt agt	624		
Gly Lys Ile Pro Ile Asp Val Asn Lys Met Asn Ile Asp Leu Leu Ser			
195	200	205	
ata tca gga cat aaa ata tat gct cca atg gga ata ggg gca tta tat	672		
Ile Ser Gly His Lys Ile Tyr Ala Pro Met Gly Ile Gly Ala Leu Tyr			
210	215	220	
gta cgt aaa cgt caa cca aga ata cga ctt act cct ata ata aat ggt	720		
Val Arg Lys Arg Gln Pro Arg Ile Arg Leu Thr Pro Ile Ile Asn Gly			
225	230	235	240
ggg gga caa gaa cgt ggt atg aga tct gga acc ata cct act cca tta	768		
Gly Gly Gln Glu Arg Gly Met Arg Ser Gly Thr Ile Pro Thr Pro Leu			
245	250	255	
gca gta ggt tta ggg gaa gca gca tat ata gct cag gaa gta atg gaa	816		
Ala Val Gly Leu Gly Glu Ala Ala Tyr Ile Ala Gln Glu Val Met Glu			
260	265	270	
gat gaa gcc att agg ata aaa gaa ttg cgt gat att tta tat agt gaa	864		
Asp Glu Ala Ile Arg Ile Lys Glu Leu Arg Asp Ile Leu Tyr Ser Glu			
275	280	285	
ata aaa aaa cat tta ccc tat gta ata ctg aat ggt gat tat gaa caa	912		
Ile Lys Lys His Leu Pro Tyr Val Ile Leu Asn Gly Asp Tyr Glu Gln			
290	295	300	
cgt ata gca gga aat tta aat tta agt ttt cca tat gta gaa gga gaa	960		
Arg Ile Ala Gly Asn Leu Asn Leu Ser Phe Pro Tyr Val Glu Gly Glu			
305	310	315	320
tct att att atg gcg att aac aac tta gca gta agt tca gga tct gct	1008		
Ser Ile Ile Met Ala Ile Asn Asn Leu Ala Val Ser Ser Gly Ser Ala			
325	330	335	
tgt aca tct gct tca cta gaa cca tct tat gtt tta cgt gcg tta aat	1056		
Cys Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Asn			

340

345

350

ata gat aag gat tta gaa cac tca tct att aga ttt gga ata ggt agg 1104
 Ile Asp Lys Asp Leu Glu His Ser Ser Ile Arg Phe Gly Ile Gly Arg
 355 360 365

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ttt act aca aaa gca gaa att tta tat gca gcg gat ctt att gta aat      1152
Phe Thr Thr Lys Ala Glu Ile Leu Tyr Ala Ala Asp Leu Ile Val Asn
          370           375           380

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agc ata aag agg ttg cgt gag atg agt cct tta tgg gaa atg gta caa      1200
Ser Ile Lys Arg Leu Arg Glu Met Ser Pro Leu Trp Glu Met Val Gln
385           390           395           400

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gaa ggt ata aat ctt aat gaa att aag tgg gat gtg cat taa 1242
Glu Gly Ile Asn Leu Asn Glu Ile Lys Trp Asp Val His
405 410

<210> 109
<211> 413
<212> PRT
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

Met Glu Lys Ile Lys Asp Ile Gln Arg His Ile Asn Leu Pro Ile Phe
1 5 10 15

Leu Asp Tyr Gln Ser Thr Thr Lys Thr Asp Ser Arg Val Leu Asp Ala
20 25 30

Met Ile Pro Tyr Phe Gln Glu Phe Ser Asn Pro His Ser Arg Ser His
 35 40 45

Cys Phe Gly Trp Lys Ala Glu Ser Ala Val Glu Leu Ala Arg Glu Arg
50 55 60

Ile	Ala	Ser	Leu	Ile	Asn	Ala	Glu	Ser	Lys	Glu	Val	Ile	Phe	Thr	Ser
65					70					75					80

Gly Ala Thr Glu Ser Asn Asn Leu Ala Ile Lys Gly Val Ala Asn Phe
85 90 95

Tyr Lys Ser Lys Gly Asn His Ile Ile Thr Val Arg Thr Glu His Lys
100 105 110

Cys Val Leu Asp Ser Cys Arg His Leu Glu Thr Glu Gly Phe Asp Val

115

120

125

Thr Tyr Leu Asp Val Gln Lys Asn Gly Ile Leu Asp Leu Asn Leu Leu
130 135 140

Lys Ser Ala Ile Thr Asp Lys Thr Ile Leu Val Ser Val Met Met Val
145 150 155 160

Asn Asn Glu Ile Gly Val Ile Gln Pro Ile Glu Glu Ile Gly Lys Ile
165 170 175

Cys His Asn His Gly Val Phe Phe His Thr Asp Ala Ala Gln Ala Phe
180 185 190

Gly Lys Ile Pro Ile Asp Val Asn Lys Met Asn Ile Asp Leu Leu Ser
195 200 205

Ile Ser Gly His Lys Ile Tyr Ala Pro Met Gly Ile Gly Ala Leu Tyr
210 215 220

Val Arg Lys Arg Gln Pro Arg Ile Arg Leu Thr Pro Ile Ile Asn Gly
225 230 235 240

Gly Gly Gln Glu Arg Gly Met Arg Ser Gly Thr Ile Pro Thr Pro Leu
245 250 255

Ala Val Gly Leu Gly Glu Ala Ala Tyr Ile Ala Gln Glu Val Met Glu
260 265 270

Asp Glu Ala Ile Arg Ile Lys Glu Leu Arg Asp Ile Leu Tyr Ser Glu
275 280 285

Ile Lys Lys His Leu Pro Tyr Val Ile Leu Asn Gly Asp Tyr Glu Gln
290 295 300

Arg Ile Ala Gly Asn Leu Asn Leu Ser Phe Pro Tyr Val Glu Gly Glu
305 310 315 320

Ser Ile Ile Met Ala Ile Asn Asn Leu Ala Val Ser Ser Gly Ser Ala
325 330 335

Cys Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Asn
 340 345 350

Ile Asp Lys Asp Leu Glu His Ser Ser Ile Arg Phe Gly Ile Gly Arg
 355 360 365

Phe Thr Thr Lys Ala Glu Ile Leu Tyr Ala Ala Asp Leu Ile Val Asn
 370 375 380

Ser Ile Lys Arg Leu Arg Glu Met Ser Pro Leu Trp Glu Met Val Gln
 385 390 395 400

Glu Gly Ile Asn Leu Asn Glu Ile Lys Trp Asp Val His
 405 410

<210> 110
<211> 414
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)...(414)
<223> Corresponds to SEQ ID NO:105, nucleotides 3375-3788
NIFU-like protein
Product = "11hworf3"

<400> 110 48
atg agt tac agt gag tct ctt cta gaa cat tat aag aat cct aaa aat
Met Ser Tyr Ser Glu Ser Leu Leu Glu His Tyr Lys Asn Pro Lys Asn
1 5 10 15

gtt ggt act tta cct aaa gag gat tac aat gta ggt act ggc tta gtg 96
Val Gly Thr Leu Pro Lys Glu Asp Tyr Asn Val Gly Thr Gly Leu Val
20 25 30

gga gct cct agc tgt ggt gat gta atg aag tta cag att aaa gta gat 144
Gly Ala Pro Ser Cys Gly Asp Val Met Lys Leu Gln Ile Lys Val Asp
35 40 45

gat aat gga aaa att ata gat gca aaa ttt aaa act ttt gga tgt ggt 192
Asp Asn Gly Lys Ile Ile Asp Ala Lys Phe Lys Thr Phe Gly Cys Gly
50 55 60

gct gca att gca gct agt tca cta gct act gag tta att aaa ggt aaa 240
Ala Ala Ile Ala Ala Ser Ser Leu Ala Thr Glu Leu Ile Lys Gly Lys
65 70 75 80

aca gta gat gag gca cat gag ttg aaa aat aca gta ttg gca aaa gaa 288

Thr Val Asp Glu Ala His Glu Leu Lys Asn Thr Val Leu Ala Lys Glu
 85 90 95

tta agt tta cct cca gtg aaa ata cat tgt tca ttt gca gaa gat 336
 Leu Ser Leu Pro Pro Val Lys Ile His Cys Ser Leu Leu Ala Glu Asp
 100 105 110

gct gta aaa gca gct ata aat gac tat cat atg aaa caa gca aac aaa 384
 Ala Val Lys Ala Ala Ile Asn Asp Tyr His Met Lys Gln Ala Asn Lys
 115 120 125

aaa aat gct act aaa gat cct aat gaa taa 414
 Lys Asn Ala Thr Lys Asp Pro Asn Glu
 130 135

<210> 111

<211> 137

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 111

Met Ser Tyr Ser Glu Ser Leu Leu Glu His Tyr Lys Asn Pro Lys Asn
 1 5 10 15

Val Gly Thr Leu Pro Lys Glu Asp Tyr Asn Val Gly Thr Gly Leu Val
 20 25 30

Gly Ala Pro Ser Cys Gly Asp Val Met Lys Leu Gln Ile Lys Val Asp
 35 40 45

Asp Asn Gly Lys Ile Ile Asp Ala Lys Phe Lys Thr Phe Gly Cys Gly
 50 55 60

Ala Ala Ile Ala Ala Ser Ser Leu Ala Thr Glu Leu Ile Lys Gly Lys
 65 70 75 80

Thr Val Asp Glu Ala His Glu Leu Lys Asn Thr Val Leu Ala Lys Glu
 85 90 95

Leu Ser Leu Pro Pro Val Lys Ile His Cys Ser Leu Leu Ala Glu Asp
 100 105 110

Ala Val Lys Ala Ala Ile Asn Asp Tyr His Met Lys Gln Ala Asn Lys
 115 120 125

Lys Asn Ala Thr Lys Asp Pro Asn Glu
130 135

<210> 112
<211> 15
<212> PRT
<213> Unknown

<220>
<223> Hypothetical sequence

<400> 112

Pro Thr Leu Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
1 5 10 15

<210> 113
<211> 13
<212> PRT
<213> Unknown

<220>
<223> Hypothetical sequence

<400> 113

Leu Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
1 5 10

<210> 114
<211> 18
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 114
cggggtaccg aattcctc

18

<210> 115
<211> 18
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 115
gcatgctcct ctagactc

18

<210> 116
<211> 9
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 116

Val Thr Ser Ser Pro Glu Gly Ser Val
1 5

<210> 117
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic peptide

<400> 117

Val Thr Ser Ser Pro Glu Gly Ser Val
1 5